GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. 6 09:37:21, 2005

OM nucleic - nucleic search, using sw model

August 26, 2005, 03:47:51; Search time 211 Seconds (without alignments) 7816.905 Million cell updates/sec Run on:

1 ggagtggaatcagtgagagg.....gtaaaaaagataataagtaa 1008 US-10-724-972A-2580 1008 Title: Perfect score: Sequence:

1202784 segs, 818138359 residues IDENTITY NUC | Gapoxt 1.0 Scoring table: Searched: 2405568 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:\*

1. /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2. /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3. /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

5. /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5. /cgn2\_6/ptodata/1/ina/bcTuS\_COMB.seq:\*

5. /cgn2\_6/ptodata/1/ina/pcTuS\_COMB.seq:\*

5. /cgn2\_6/ptodata/1/ina/pcTuS\_COMB.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di		_	SOFTER	
Result No.	Score	Query Match	Length	QB	ID	Description
1	222.6	22.1	999	4	US-08-956-171E-355	Sequence 355, App
8	222.6	22.1	668	4	US-08-781-986A-355	355,
m	162.2	16.1	242	4	US-08-956-171E-2556	2556,
4	162.2	16.1	242	4	US-08-781-986A-2556	Sequence 2556, Ap
'n	158.2	15.7	183	m	US-09-1:34-001C-2023	
9	125.4	12.4	2115	4	US-08-956-171E-604	604,
7	125.4	12.4	2115	4	US-08-781-986A-604	604,
60	124	12.3	666	4	US-09-830-217-15	15, A
6	124	12.3	666	4	US-10-278-946-15	15, A
10	124	12.3	3775	4	US-08-956-171E-238	Sequence 238, App
11	124	12.3	3775	4	US-08-781-986A-238	
12	109.4	10.9	3046	4	US-09-710-279-3782	Sequence 3782, Ap
13	77.2	7.7	1056	4	US-09-543-681A-2690	
c 14	73.8	7.3	421	4	US-08-956-171E-383	383,
c 15	73.8	7.3	421	4	US-08-781-986A-383	٠.
16	72.2	7.2	612	4	US-09-902-540-1357	1357
17	70.6	7.0	975	m	US-09-071-035-37	Æ.
18	70.6	7.0	984	4	US-09-134-000C-937	Sequence 937, App
19	69.8	6.9	709	4	US-09-902-540-1583	1583,
20	68.8	6.9	702	4	US-09-902-540-2208	2208
c 21	68.8	6.9	7218	Н	US-08-232-463-14	14,
22	65.6	6.5	883	ص -	US-09-071-035-39	
c 23		6.4	3153	4	US-09-710-279-3348	
24	64.6	6.4	3267	4	US-09-710-279-4042	404
25	64.6	6.4	3618	4	US-09-710-279-3564	3564,
26	64.4	6.4	1044	4	US-09-710-279-461	
27	64.4	6.4	1044	4	US-09-710-279-1267	Sequence 1267, Ap

	Sequence 1280, Ap	Sequence 22, Appl	Sequence 1393, Ap	Sequence 37, Appl	Sequence 37, Appl	75,	Sequence 13, Appl	Sequence 1, Appli	Sequence 66, Appl	Sequence 14624, A	'n	Sequence 1, Appli	Sequence 1, Appli	Sequence 3335, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 862, App	
US-09-134-001C-2655	US-09-902-540-1280	US-09-806-708B-22	US-09-543-681A-1393	US-08-956-171E-37	US-08-781-986A-37	US-09-601-198-75	US-08-487-826B-13	US-09-790-988-1	US-09-601-198-66	US-09-949-016-14624	US-09-902-540-1318	US-08-916-421B-1	US-09-692-570-1	US-09-134-000C-3335	US-08-559-896B-1	US-09-351-794A-1	US-09-107-532A-862	
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6.4	6.3	6.2	6.2	6.1	6.1	5.9	5.9	5.9	5.8	2.6	2.0	9.6	5.6	5.5	5.5	5.5	5.4	
64.4	63.6	62.2	62	61.8	61.8	59.8	59	50	58.8	56.8	56.4	56.4	56.4	55.2	55	55	54.8	
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## ALIGNMENTS

RESULT 1 US-08-956-171E-355 Sequence 355, App. Sequence 355, App. Sequence 355, App. STAT COURESPON STAT COURTER SOFT COMPUTER COURTER SOFT COMPUTER SOFT COMPUTER SOFT SOFT SOFT SOFT SOFT SOFT SOFT SOFT
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us-10-724-972a-2580.rni

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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
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                                                                                   Gaps
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                                          DB 4; Length 668;
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                                                                                   94;
                                        Score 222.6; DB 4
Pred. No. 8.3e-39;
0; Mismatches 94
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COMPUTER: HP Vectra 486/33
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIPICATION > CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2556, Application US/08956171E patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Charles Kunsch
Gil H. Choi
                                        Query Match 22.1%;
Best Local Similarity 74.8%;
Matches 279; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Disket
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STATE: Maryland
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US-08-781-986A-355
US-08-781-986A-355
I Sequence 315, Application US/08781986A
Patent No. 6773-724
I Patent No. 6773-724
I GENERAL INFORMATION:
APPLICANT: Charles Kunsch
I TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREST: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                       627 TTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAAGGTTTTAA
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  Length 668;
                                            94; Indels
  DB 4;
Score 222.6; DB 4
Pred. No. 8.3e-39;
0; Mismatches 94
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HV Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INPORMATION:
TELEPAX: (301) 309-8504
TELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/781,986A
  22.1%;
74.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            987 TAGTAAAAAGAT 999
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TYPE: nucleic acid
STRANDEDNESS: double
Query Match 22.1
Best Local Similarity 74.8
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA
APPLICATION NUMBER: U
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                            ; TOPOLOGY: 1:
US-08-781-986A-2556
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                                                                                                                                                                                                                                                                                                                                           122 CAGCCAAACTTAGAAATTAGTAAATTAAAACCGGATTTAATTATGCTGGTGATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2556, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       388 AGACACAAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                       328 CAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAAT
                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                           Score 162.2; DB 4; Length 242; Pred. No. 6.4e-26; O; Mismatches 50; Indels 0
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                  INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISICS:
LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                     TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
                                                                                                                                                                                              Query Match
Best Local Similarity 79.3%;
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 T 448
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               906 CCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     846 AAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGA
                                                                                                                                        2 GATGCATTAGCAGCATTAGACGTTAAACCAGTTGGTATTGCTGATGATGGTAAAAAA
                                                                                                                                                                                                                                                                                                                   328 CAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAAT
                                                                                                                                                                                                                                                                                                                                                 208 GATGCGTTAGTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAT
                                                                                                                                                                                                              268 CGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAG
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     Length 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.7%; Score 158.2; DB 3; Best Local Similarity 98.2%; Pred. No. 4.3e-25; Matches 160; Conservative 0; Mismatches 3;
Score 162.2; DB 4;
Pred. No. 6.4e-26;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2023, Application US/09134001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-956-171E-604
; Sequence 604, Application US/08956171E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus epidermidis US-09-134-001C-2023
        16.1%;
                             Best Local Similarity 79.3
Matches 191; Conservative
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458 ATTATAATGAAAATATTGATGCTTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAG 517
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301 ATGAAGAACTTGCCAATATCAATCCAAAAGTTATGATTTTAGCCACTGACGGAAAAACGG 360
                                                                                                                                      878 TGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAA 937
                                                                                                                                                                            415 TGAAAGATAACAAAGTTTATGACGTTGACATAAGTGAGTTGAAATCAAGGGGGATTA 474
                                                                                                                                                                                                                                 938 TITCITCAGAAGAAATGGCAAAAGAACTIGITGAATTATCTAAGAAAGATAGTAAAAAG 997
                                                                                                                                                                                                                                                                     475 TCGCAAGTGAAAGTATGGCAGAAGATTTAGAAAAATTGCAGAAAAAGCAAAATAAAAAT 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 604, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TILLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATTATAATGCAAATATTGAAGCATTTAAAACAGTCGCTAAAGCAGTAGGCAAAGAGAAAG
                                               818 CTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTG
                                                                                        361 ACAAAAA-----TAGAACGAAATTCATTGATCCTGCAGTTTGGAAATCATTAAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 125.4; DB 4; Length 2 Pred. No. 8.1e-18; 1; Mismatches 247; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
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REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
12.4%;
Best Local Similarity 53.2%;
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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US-08-781-986A-604
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                                                                                                         Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698 GTGATGATGTTACTAAAGGTTTAAGTAAGTATCTTAAAGGACCTTACTACAAATGAACA 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIGAAACITTATCTCAAGTGAATCCTGAGCGTATGTTCATAATGACAAAGCAAGGTT 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 AAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATATAAAAAAGAAATAA 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAGGCGAGAAGCGTCTGGAAAAGCATGATAAAATATTAGCGGAGATTAGAAAAAAATTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AACAGAGTÁCGTTAAAÁTCTGCÁTŤTGCATTCGGTATCTCAÁGÁGCÁGGTATGTTTATTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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MEDIUM TYPE Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: Diskette, 3.50 inch, 1.4Mb storage
MEDIUM TYPE Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIPRACATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 125.4; DB 4; Length:
Pred. No. 8.1e-18;
1; Mismatches 247; Indels
                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REPERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 604: US-08-956-171E-604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
                                                                          Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2115 base pairs
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.2%;
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                         CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623 CAGGITTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605 rccer---gcrearcaracarearrrargcresresrargcresresrearerraare 661
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                                                                                                                  267 TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 TGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAA
                                                 198 rdaccrccrcraractrraccrcraraccrcraccrcracaarcarcacaaa
                                                                                                                                                                                                                                                                                                                                                                         TAGACACAAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tagaaatgaaaagtrtacgatcaattatctaaatcgcacc------AACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCGATGGAGATTATAATGAAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAG
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; Facent No. 6821754
; GENERAL INFORMATION:
; APPLICAMT: Simpson et al.
; TILE REFERENCE: PB461USD1
; CURRENT APPLICATION NUMBER: US/10/278,946
; CURRENT FILING DATE: 2001-0-24
; PRIOR APPLICATION NUMBER: US 09/830,217
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 06/080,217
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1998-03-18
; PRIOR FILING DATE: 1998-03-03
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: US 60/080,296
; PRIOR APPLICATION NUMBER: US 60/080,4674
; PRIOR APPLICATION NUMBER: US 60/080, 296
; PRIOR APPLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        803 CAAACAAAGCAAGTTCTAACGAACCTTCACTA 834
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; ORGANISM: Staphylococcus aureus
US-10-278-946-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-10-278-946-15
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      ATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAA
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; Sequence 15, Application US/09830217
; Patent No. 6521441
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
; TILE REFERENCE: P8461PCT
; CURRENT APPLICATION NUMBER: US/09/830,217
; CURRENT APPLICATION NUMBER: 00/080,296
; PRIOR APPLICATION NUMBER: 60/080,296
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1998-06-07
; RIOR APPLICATION NUMBER: 60/084,674
; PRIOR FILING DATE: 1998-05-07
; SOFTWARE: PatentIn Ver. 2.0
; SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 1.4e-17;
0; Mismatches 380; Indels
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12:3%;
Best Local Similarity 50.7%;
Matches 412; Conservative
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US-09-830-217-15
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INFORMATION FOR SEQ ID NO: 238 SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                                          CITY: Rockville
STATE: Maryland
COUNTRY: USA
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Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
G11 H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
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                                                                                           AATTAAAATGCTTGTTGTTACGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGAA
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   Length 999
 Score 124; DB 4; Length 99;
Pred. No. 1.4e-17;
0; Mismatches 380; Indels
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Query Match
Best Local Similarity 50.7
Matches 412; Conservative
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US-08-956-171E-238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 aairiaaaangcingrigtracgcingcinicciacriferrmagcagargragragagaa
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                                                                                                                                                                                                                                                                                   storage
                                                                                                                                                                                                            ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPEs Diskette, 3.50 inch, 1.4Mb stc
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%; Score 124; DB 4; I
50.7%; Pred. No. 1.8e-17;
tive 0; Mismatches 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION UNMERR. 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 238:
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Scien
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8439
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764 rccaactracarcraaagaaagcatrccarraargaacgcrgarcararrifrgragraa 823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704 ATTTAGGATTCAAACGTAATAAAGACTTACAAAAACAAGTTGATAATGGTAAAGGATATTA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     743 ACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAATGA 802
60 AATTAAAATGCTTGTTACGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA 119
                                                                 TAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA 146
                                                                                                         trcaaaraaacaarcarcrearaacaaagaraagaaaaacaacrrcaarraaacardcaar 179
                                                                                                                                                                                               180 gegracakorgaaarraaagggaaaccaakoccrcriterrackrararcaagraccac 239
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                                                                                                                                                                                                                                                                                                                                       TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA 326
                                                                                                                                                                                                                                                                                                                                                                                 300 ACCGAAATTCGAATACATAAAAATGATTAAAAGATACTAAGATTGTAGGTCAAGAACC 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 TGCACCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCAAAAGT 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGAAATGAAAAGITTACGATCAATTATCTAAAATCGCACC-------AACAG 466
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Facent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT PILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ. ID NOS: 44772
SOSTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAGA---AATAACTATGGATAAAATCAAAAGGTATTGCCTGCAGTAGCTGCTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGITTGCTTGCTCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTT
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                                                                                                                                                                                                                                                TGATGCGTTAGTTGCTTTAGATGTTAAAACCTGTTGGGATAGCGGATGATAACAAAAAAA
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US-09-710-279-3782
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LENGTH: 3046
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Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
CCUNTRY: USA
                                GTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATATA 565
                                                                                                                                                                                                             623 CAGGITIGCTIGCICATCCAAGCAACTCTIAIGTIGGICAATICCIAAGICAACIAGGIT 682
                                                                                                                                                                                                                                         704 ATTTAGGATTCAAACGTAATAAAGACTTACAAAAACAAGTTGATAATGGTAAAGATATTA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                    764 rccaáctrácarcráaagaáagcarrccarráargáacgcrágarchrarritrgrágraa 823
                                                                        527 GGAAAGAAAAGAAGCTGAAGATTTACTTAAAAAGTACGATGATAAAGTAGCTGCATTCC
                                                                                                                                                          587 AAAAGATGCAAAGCAAAGTATAAAGATGCATGGCCATTGAAAGCTTCAGTTGTAACT
                                                                                                                       AAAAAGA---AATAACTATGGATAAAATCAAAAGGTATTGCCTGCAGTAGCTGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   803 CAAACAAAGCAAGTTCTAACGAACCTTCACTA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             824 AATCAGATCCAAATGCGAAAGATGCTGCATTA 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE:
CLASSPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
TELEPHONE: (301) 309-8512
TELEPHONE: (301) 309-8512
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid_
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-781-986A-238
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Best Local Simi
Matches 412;
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27 AATTITAAGIGIAATIGGCITATIGITITGTITIAATIGCAACIGCAGCAIGIGGAAATAA

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Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
CORRESPONDENCE ADDRESS:
                                             TITAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGA 560
                                                                                         582 TTTTGGTAAAGAAGAACAAGCTAAAAATTATTAGCTGACTTCAATAGCAAAATTGATAC 641
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522 TATCGACAGCACACGCTTTATTGACAGCCTCACTGAGCGTACAACGACTTTAGGTCAAAT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.3%; Score 73.8; DB 4;
61.9%; Pred. No. 7.1e-07;
7ative 0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILLING DATE: 20-0ct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILLING DATE: January 3, 1996
APPLICATION NUMBER: 08/781,986
FILLING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLOMANE: Mark J. Hyman
REGISTRATION NUMBER: 46,789
RESPERENCE/DOCKET NUMBER: PB248P1
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 314-1224
TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear sequence SEQID NO: 383: US-08-956-171E-383
                                                                                                                                                                                                                                                                                                      Sequence 383, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 421 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-8
INFORMATION FOR SEQ ID NO: 383
                                                                                                                                                                                     642 GGTAAAAGCAAAAA 655
                                                                                                                                            561 ATATAAAAAAGAAA 574
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Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
                                                                                                                                                                                                                                                             RESULT 14
US-08-956-171E-383/c
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APPLICANT: GARY BRETON
TITLE OF INVENTION: UDGOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1909-04-05
PRIOR REPLING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 AGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGTTGAGTATTCATT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 TCAAGGCACCACTGAGATCCCTGCTCACCACAAAAGTGGTTGTGATGAACATGGAAC 284
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                            ; FEATURE:
) OTHER INFORMATION: Description of Artificial Sequence: synthetic
) OTHER INFORMATION: nucleic acid sequence
08-09-710-279-3782
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                                                                                                                                         Length 3046;
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                                                                                                                                                                                                                                     1 GGAGTGGAATCAGTGAGAGGTTTAAAAATTTTAAGTGTAATTGGCTTAT
                                                                                                                                                                                         Indels
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                                                                                                                                         DB 4;
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0; Mismatches 278;
                                                                                                                                         Score 109.4; DB 4
Pred. No. 2.4e-14;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2690, Application US/09543681A
Patent No. 6605709
                                                                                                                                         Query Match
Best Local Similarity 95.0%;
Matches 113; Conservative
       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Proteus mirabilis
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SEQ ID NO 2690
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US-09-543-681A-2690
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TYPE: DNA
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127 GTTGAAATCAAGCACGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTT 186
                                                                                                                                                                             US-08-781-986A-383/C

Sequence 383, Application US/08781986A

Sequence 383, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland

STATE: Maryland

COUNTRY: USA
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                                  85 ATTTCGGTAAAAGATGAAAATGGTACAGTAAAAGTACCTAAAGATGCAAAACGTATCGTT
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61.9%; Pred. No. 7.1e-07;
tive 0; Mismatches 72; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INPORMATION:
TELEFAM: (301) 309-8514
INFORMATION FOR SEQ ID NO: 383:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Matches 117; Conservative
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                                                                        187 GTTCTTGAG 195
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RESULT 16

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GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
TITLE OF INVENTION: Experiment of the conference of the correspondence ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 ATAACAAAAAATCGTATTATTAACCATTAAGAGATAAAATTGGAAAATACACTTCTG 313
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wigh Mycoccus continue Genome Sequences and Uses Thereof TITLE OF INVENTION: Mycoccus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 TIGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAATAAAATTGCTCCTACGA
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Pred. No. 1.7e-06;
0; Mismatches 170; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(612)
COTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
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Sequence 1357, Application US/09902540 Patent No. 6833447
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Patent No. 6448043
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Best Local Similarity 50.4%;
Matches 173; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1357
LENGTH: 612
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NAME/KEY: unsure
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US-09-134-000C-937
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                                                                                                                                                                                                                                                                                                                                                                                    7.0%; Score 70.6; DB 3; Length 975;
48.8%; Pred. No. 4.1e-06;
tive 0; Mismatches 314; Indels 1
                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDENESS: double
SUFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 48.8
Matches 317; Conservative
                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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RESULT 18

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DEPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 ATCAACGAAACAAAATATCGAAACGTTAGGCACTATTTTTGATAAGAAGAGGTAGCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 70.6; DB 4; 148.8%; Pred. No. 4.1e-06; tive 0; Mismatches 314;
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2-09-902-540-1583
; Sequence 1583, Application US/09902540
; Patent No. 6833447
Sequence 937, Application US/09134000C Patent No. 6617156 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.8
Matches 317; Conservative
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; TYPE: DAMA; ORGANISM: MYXOCOCCUS Xanthus US-09-902-540-2208
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 AAGCGAGCCAAGCTTAGAAGCAATCGCTGTTAAAAGCCTGACTTGATTATCGGAAATAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 TAATAGACACAAAGGTATTTATAAAGACTTAAATAAATTGCTCCTACGATTGAACTGAA 443
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: Misgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFRERNCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2208
LENGTH: 702
                 APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 103/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGCTGCGCGCGAGATTGGAAATCAAAC-----TTTAAGCTATATGCAAAAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                             Length 709;
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Patent No. 6833447
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.9%;
Matches 210; Conservative
                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Myxococcus xanthus
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US-09-902-540-2208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            565 AAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTGAAATCA
                                                                                                                                                             1 AATCCGCGGTTTGACCATATTAAAGGTCAGATGAAAGGCGTTAAAAGTGTGGGTACAGAA
                                                                                                                                                                                                                     325 AAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTGCTGATAAT
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                                                                                                          265 AATCGTATTATAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGT
                                                        Gaps
                                                        9
Length 702;
                                                        Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 21
US-08-232-463-14/C
S-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LATGHER
Score 68.8; DB 4;
Pred. No. 9.4e-06;
0; Mismatches 202;
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REPERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
     Query Match
Best Local Similarity 49.8%;
Matches 209; Conservative
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FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-071-035-39
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Patent No. 6448043
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 ATTIGITGAIGCGIIAGITGCIIIAGAIGIIAAACCIGIIGGGAIAGCGGAIGAIAACAA 260
                                                                                                                                                                                                                                                                                261 AAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAAC 320
                                                                                                                                                                                                                                                                                                                                        321 ACGTAAGCAACCTAACTTAGAAGAATCAGTAAACTTAAACCAGATTTAATTATTGCTGA 380
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                                                                                                                                                                       Query Match
6.8%; Score 68.8; DB 1; Length 7218;
Best Local Similarity 4.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 235; Mismatches 147; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 ATATAAAAAGAAATAACTATGGATAAAAATCAAAAGG 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFWARE: ASCII Text CURRENT APPLICATION DATA:
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
       TELEFAX: (703)683-4109
TELEFAX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PIZSPL-F18
US-08-232-463-14
(703)836-9300
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MEDIUM TYPE: Diskett
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TELEPHONE:
TELEFAX: (
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US-09-071-035-39
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US-09-710-279-3348/c
US-09-710-270-3348, Application US/09710279
Sequence 3348, Application US/09710279
Sequence 3348, Application US/09710279
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 CAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAG
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Pred. No. 4.8e-05;
0; Mismatches 284; Indels 18;
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9B369P2
TELECOMMUNICATION INFORMATION:
TELEPRONE: (301) 309-8514
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.3%;
Matches 294; Conservative 0
                                                                                                                                                                                                                                                                          LENGTH: 889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                         linear
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                       1006 T 1006
                                                                                                      243 T 243
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LENGTH: 3267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 AACAAGCAGAATCCAGATGTTATTTAGCTATGGATCGTGGTTCAGTTGTAGGTAAA 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    829
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                                                                                                                                                                                                                                                                                                                                               GTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGT-----TAAA
                                                                                                                                                                                      Gaps
                                                            ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-31348
                                                                                                                                                                                    30;
                                                                                                                                                       Length 3153;
                                                                                                                                                    Query Match 6.4%; Score 64.6; DB 4; Length 3 Best Local Similarity 47.0%; Pred. No. 0.0001; Matches 452; Conservative 0; Mismatches 479; Indels
SOFTWARE: Patentin Ver.
SEQ ID NO 3348
LENGTH: 3153
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                                                  TYPE: DNA
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Fatent No. 6703492
GENERAL INFORMATION:
APPLICANT: KINMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
FRIOR APPLICATION NUMBER: 60/164,258
FRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ. ID NOS: 4472
SOFTWARE: PATENTIN VOY: 2.1
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Best Local Similarity 47.0%; Pred. No. 0.0001;
Matches 452; Conservative 0; Mismatches 479; Indels 30;
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT PILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 1999-11-09
NUMBER OF SIEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
CTAAAAAGGTTTACCTAAAAGGTGAAAATAACCAATCTTTACCTAAATTTTTAGATGAATTT
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US-09-710-279-461
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Patent No. 6703492
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PLILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
    TTTGGACCAGGAGGAGATTTGGTGGTTTAGTGTTTGATACATTAGGATTTAAACCTGCA
                                               ACTAAAGACTTTAATAAGAAAGTAATGTATTTÄTTGGTTAACGAAGGTGAACTATCAACG
                                                                                          TCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGTT
                                                                                                                                                                                1457 GACAAAAAGGTTAGCAAAAGCCCGCATGGTC-----AAAATATAAATAATGAATATT
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US-09-710-279-3564
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                                                                                                                          Gaps
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
                                                                                                                        30;
                                                                                    Length 1044;
                                                                                  Query Match 6.4%; Score 64.4; DB 4; Length 1 Best Local Similarity 47.1%; Pred. No. 9e-05; Matches 450; Conservative 0; Mismatches 476; Indels
                                                      US-09-710-279-461
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                                                                                                                                            AND PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1044;
                                                                                                                    APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.4%; Score 64.4; DB 4; Length 10.
Best Local Similarity 47.1%; Pred. No. 9e-05;
Matches 450; Conservative 0; Mismatches 476; Indels
                                             Application US/09710279
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
                                               Sequence 1267, Applic
Patent No. 6703492
GENERAL INFORMATION:
RESULT 27
US-09-710-279-1267
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Pater
SEQ ID NO 1267
LENGTH: 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1280, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: FILING NUMBER: US/09/902,540
CURRENT FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
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                                                                                                                                          823 AACAAGCAGAATCCAGATGTTATTTTAGCTATGGATCGTGGTTCAGTTGTAGGTGGTAAA
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                                       AATATTGATGCTTTTAAAACAATTTCAAAAGCTTTTAGGTAAAGAAGAAGAAGGTAAAAAA
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48.1%; Pred. No. 0.00013;
iive 0; Mismatches 191; Indels 0
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; OTHER INFORMATION: unsure at all n locations US-09-902-540-1280
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SEQ ID NO 1280
LENGTH: 1039
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Matches 177; Conservative
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US-09-902-540-1280
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Referent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: REPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: REPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT PILING DATE: 1998-08-13
PRIOR PELICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PELING DATE: 1997-08-14
RIOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674
SEQ ID NO 2655
LENGTH: 1056
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                                                                                                                                                                                         GCAACAACAACTCAAGTTTTAAAAAACAAAGTTATAAAAAATGTAAAAAGCAGTAAAAAGT 930
                                                                                                                                                                                                                               CAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCA 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTGATTCTAAAGAAACTGTAACCATCAAAAATAGTTTTGAAGCAAGTGGTAAAAGAAAAT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGTTGGGATAGCGGATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGA---T 291
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                                                                                                                                                                                                                                                                    931 AATCATATTTACGAATTAGATCCAAAACTATGGTATTTCTC-----TTCAGGATCTTCA 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 AATGGCAGTGATAAGAAAAATCTCTAATACTGTCGAAGTACCAAAGAATCCTAAAAT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGATGATAAGTATATTAATACTGGAAATTTAAAAGAAGTGAACTTTGATAAAGTTGCA 411
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                                                                                                                                                                                                                                                                                                                               985 ACGACAACTATCAAACAAATAGATTAAATGAAGTAGTAGAGAAAGTTGAAAA 1040
                                                                                                                                                                                                                                                                                                       61 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAA
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     GACAAAAAGGTTAGCAAAAGCCCGCATGGTC----AAAATATAAATAAATATATATT
                                                                            AACAAGCAGAATCCAGATGTTATTTTAGCTATGGATCGTGGTTCAGTTGTAGGTGGTAAA
                                                                                                                                                      CCTTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAAACGCTGTGAAAAT
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Pred. No. 9e-05;
0; Mismatches 476; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Staphylococcus epidermidis US-09-134-001C-2655
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Best Local Similarity 47.1%;
Matches 450; Conservative (
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Sequence 1393, Application US/09543681A

Batent No. 6605709

BAPENT OF ARX PRETON

APPLICANT: GARX BRETON

TITLE OF INVENTION: DIGGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09
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310 TCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTA 369
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                                                                                                                                                                                                                                                          699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 MWWMDHMNTHCTYGNNTWGSAYBMAAMSMWAAGASNBVTYNWCWRMTYMGKTMTNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XAWYYRTKTVAWCNNRYYYDTAVWTBKRNYKYCYAYBWYYBMYMGKHHWBWWRRAABHRSW
                                                                                                                                                                           | | : : : | :: :::::| | | ::::| | : ::::| | 637 CCTCTRMPITMEWTMKGDGMTVRKKVKWRDTTCTYVDVWADSWVWWXANWMRCRDV-TYTR
                                                                                                                                                                                                                                                                                                                                                                                       GTAGCTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTA
                                                                                                                                                                                                                                                                                                                AAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCA
                                                                            ACGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACA
                                      KTWMNTWYWDMMTTMBTTTTTRNMTTSTNMTNNNNNMWACTNNNNNMWKAYYAHATNNW
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Pred. No. 0.00029;
0; Mismatches 250; Indels
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Best Local Similarity 47.1%;
Matches 225; Conservative
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SEQ ID NO 1393
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US-09-543-681A-1393
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                                                                                                                                                                                                                                                                          567
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                                                                                                                                                           434 TIGAACIGAAAAGITICGAIGGAGAITATAAIGAAAATATIGAIGCITITAAAACAAITI 493
                                                                                                                                                                                                 554 TIGAAGAATATAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAG 613
                                                                                                                                                                                                                                                                                                                                      10 TCAGTGAGAGGTTTAAAAATTTTAAGTGTAATTGGCTTATTGTTTTGTTTTAATTGCAACT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NS-09-006-708B-22/C

Sequence 22, Application US/09806708B

Patent No. 67844313.

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTYON: Regulation of Embryonic Transcription in Plants

FILE REFERENCE: 4810-58741

CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT APPLICATION NUMBER: US 60/147,133

PRIOR PILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0

SEQ ID NO 22

LENGTH: 1141
                                          494 CAAAAGCTTTAGGTAAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
        TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA
                                                                                GapB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: [1)..(1141); CTHER INFORMATION: Consensus sequence of A.t., L.a., and B.n. FAEL US-09-806-708B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   628 ATATAÀÀ 635
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291 TAAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAG 350
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US-08-781-986A-37

US-08-781-986A-37

Sequence 37, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 rgaaricaaaaagcrgcaccraaagcgaaarrgrrrargrrgcrgcagargaaaagaa 207
                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCGACGAAACCCGAAGTAATCTTTATCTCTGGACGTACAGCTAATCAAAAGAATTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 cttaattiggitcaatgaaacaaaacactgaaaatatcggaaaaatttacga---taaaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 AGATAAAGCTAAAGAATTAAATAAAGATTTAGATAACAAAATTGCTTCAATGAAAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAACTGCGAAACAAGCATTAAATAATCCTGTATTAAAAAAAGTTAAAAGCAATTAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    885 TCAACGIGITGATATITIAGACCGIGACTTAIGGGCAAGAICACGIGGTTTAATITICTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             619 AGACAAAGTATATATATTTAGATCCTAAATTATGGTACTTTGCAGCTGGATCAACTACAAC
                                                                                                                                                                                                                                                                                                                                                TAAAGATGATAAATATACAAACGTTGGTAATTTAAAAGAAGTGAATTTGATAAATTGC
                                                                                                                                                                                                                                                                                                                                                                                              351 TAAACTTAAACCAGATTTAA---TTATTGCTGATAATAATAGACACAAAGGTATTTATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 AAATATTGATGCTTTTAAAACAATTTCAAAAGCTTTTAGGTAAAGAAGAAGAAGTAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 TGATAAAAAGTAAGTAATAGCAATCATGGACA-----AAATGTTTCTAACGAATATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       768 ATCTCAAGTGAATCCTGAGCGTATGTTCATAATG---ACAAACAAAGCAAGTTCTAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 TAATAAAGAAAATCCAGATGTTATTTTAGCGATGGATAGAGGTCAAGCGATAAGTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825 ACCTTCACTAAAAGAACTAGAAAAAAGATCCTGTATGGAAGAAATTAAAACGCTGTGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACTTAAAATAAAATTGCTCCTACGATTGAACTGAAAAGTTTCGATGGAGATTATAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               679 TACAATTAAACAAATTGAGGAACTTGATAAAGTTGTAAAATAATTTTAAAA 729
                                                                                                                                                                                                                   Length 9834;
                                                                                                                                                                                                                 Score 61.8; DB 4;
Pred. No. 0.00052;
0; Mismatches 362;
                                                                                                                                                   37:
                                                                                                                            TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO:

US-08-956-171E-37
           INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 9834 base pairs
                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                   6.1%;
                                                                                                                                                                                                                                   Best Local Similarity 47.0 Matches 334; Conservative
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Patent No. 6593114

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barseh
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE
                                                                                                                                                                                                                                                                 335
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                                                                                                                                                                          AGTIGCATTAGGITT --- AGCGGATAAAGTGGTTGGTTTACCATTAGGAAATGCACCTGA 293
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                                TAATCAAATIGTTGAACAGCAAAATGATAAAGTTGTTATCAAGCACCTATTAGGTGAAAC
TAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTAC
                                                                                     GAAAGTACCTAAACACCCTAAACGTGTTGTTCTTGAGTATTCATTTGTTGATGCGTT
                                                                                                                              177 TGCAĞTATCTAAAATCCGTCTAAGGTTĞTACTGTTTĞATTTTGGTCTATATGACTCTTT
                                                                                                                                                                                                                                                                 TAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Dishette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: January 5, 1996
APPLICATION WUBBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Scier
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
US-08-956-171E-37
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APPLICANT: Chen, Ellson Y.
APPLICANT: Chen, Ellson Y.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
TITLE OF INVENTION: UNCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA; TITLE OF INVENTION: UNEALYTICUM
TITLE OF INVENTION: UNEALYTICUM
TITLE OF INVENTION: UNBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAATTAATGGTATTCATACAGAAGTTGTTCAAGATAAATATGGTAAAAATACATATAA 3794
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                                                                                                            AAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGA
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885 TCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59.8; DB 4; Length 5 Pred. No. 0.0013; 0; Mismatches 302; Indels
                                                                                                                                                                                                                                                                                                                                                  ; Sequence 75, Application US/09601198
; Patent No. 6531583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Ureaplasma urealyticum US-09-601-198-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.9%;
Best Local Similarity 44.4%;
Matches 241; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         RESULT 34
US-09-601-198-75/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akcgadadactricaataaaactigitatgtatritaktagtriaacgaaggtigaattatcaac 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 TAAACTTAAACCAGATTTAA---TTATTGCTGATAATAATAGACACAAAGGTATTTATAA 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      825 ACCTTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAA 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 TAAAGATGATAAATATACAAACGTTGGTAATTTAAAAGAAGTGAATTTTGATAAATTGC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 reaarircaaaaagcrececeraagcgaaaarrerrrarerregecagargaaagaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648 CTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 ATTIGGACCIAAAGGICGITITIGGIGGATIAGITITACGATACATIAGGAITICAAIGCAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HV Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
COFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.1%; Score 61.8; DB 4; 1
Best Local Similarity 47.0%; Pred. No. 0.00052;
Matches 334; Conservative 0; Mismatches 362;
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BENEON, BOD
REGISTRATION NUMBER: 30,446
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-85.4
TELEFAX: (301) 309-85.4
TELEFAX: (301) 309-85.4
TELEFAX: (301) 309-85.4
TELEFAX: (301) 309-85.5
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 9834 base pairs
                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
               : 9410 Key West Avenue
Rockville
                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                Maryland
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430 ACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACA
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49.6%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09790988; Patent No. 6632935; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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US-09-790-988-1
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US-09-790-988-1
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APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: S
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Pred. No. 0.0024;
0; Mismatches 170; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ENDORY disk
COMPUTER: ENDOR COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGRAT INFORMATION:
NAME: Israelsen, Ned
REFERENCZ/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COUNTRY: US
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Patent No. 5993827
GENERAL INFORMATION:
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INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.1%;
Matches 173; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-487-826B-13
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US-08-487-826B-13
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                                                                                                                              315 AGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTAT
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                                                                  ATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAAACGCTTAGAAGAACACGATAAG
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APPLICANT: WATANNE, HIDEMI
APPLICANT: WATANNE, HIDEMI
APPLICANT: WATANNE, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR PILLING DATE: 2000-04-07
                                                                                                                                                                                                                                                             15868 AAATAAAAAATTTAATTAAATAAAAAAATTAAAAAATTTAA 15912
                                                                                                                                                                                                 550 AAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAA 594
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SEQ ID NO 1318
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-414
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Leffkowitz, Elliot
TITLE OF INVENTION: UNCLEIC ACID PROBES AND METHOD FOR DETECTING URBAPLASMA
TITLE OF INVENTION: URBALYICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR APPLICATION NUMBER: 60/073,189
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 861
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Sequence 14624, Application US/09949016
Patent No. 6812339
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US-09-601-198-66
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Best Local Similarity 44.8%;
Matches 225; Conservative
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REPERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 GGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 TATICATITGITGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AACAAAAAAATGGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 CGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.2%; Pred. No. 0.011;
Matches 193; Conservative 0; Mismatches 202; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136900 TAATATAAATATATATAACTAATATATAAATATATA 136861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 AAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAA 590
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LOCATION: (1)..(614)
OTHER INFORMATION: ungure at all n locations
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-100-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14624
LENGTH: 147382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1118, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION: APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(147382)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(14738;
                                                                                                                                                                                                                                ORGANISM: Human
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LOCATION: (234187). (234187)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (234220). (234220)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (234814).
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t.
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                                 KEY: misc feature
TION: (103998). (103998)
INFORMATION: n equals a,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
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LOCATION: (559241) ..(559241)
OTHER INFORMATION: n equals a,
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a,
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
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COCATION: (312837)..(312837)
THER INFORMATION: n equals a,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                       ION: (98343)..(98343)
INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (657081). (657081)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
                                                                                                         LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals
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LOCATION: (98343)..(98
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19-08-916-421B-1/c

1 Sequence 1, Application US/08916421B

1 Patent No. 6503729

1 GENERAL INFORMATION:

APPLICANT: Bult et al.,

1 TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729

1 TITLE OF INVENTION: jannaschii

1 TITLE OF INVENTION: jannaschii

1 TITLE OF INVENTION: jannaschii

1 TILLE OF INVENTION: jannaschii

2 TILLE OF INVENTION: jannaschii

3 TILLE OF INVENTION: jannaschii

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8 TILLE OF INVENTION: jannaschii

9 TILLE OF INVENTION: jannaschii

1 TILLE OF INVENTION: jannaschii

1 TILLE OF INVENTION: jannaschii

1 TILLE OF INVENTION: jannas
                                                                                                                                                              251 ATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTT 310
                                                                                                                                                                                                                                                                     311 CTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAA 370
                                                                                                                                                                                                                                                                                                                          CGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAA 490
                                                                                                                                                                                                                360 CAŻARAŻCĄCZĄCZĄRARAZĄZĄTŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻ
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                                                  5.6%; Score 56.4; DB 4; Length 614;
47.7%; Pred. No. 0.0042;
tive 0; Mismatches 181; Indels
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LOCATION: (28222)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (28257) ..(28258)
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a,
                                                                             Best Local Similarity 47.7
Matches 165; Conservative
  US-09-902-540-1318
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                                                       Query Match
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Score 56.4; DB 4; Length 1664976;
Pred. No. 0.022;
0; Mismatches 216; Indels 8;
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; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1313224). (1313224)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1349473). (1349473)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc feature
LOCATION: (779455). (779455)
NAME/KEY: misc feature
LOCATION: (779455). (779676)
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OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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Best Local Similarity 47.7%;
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LOCATION: (855539)..(855539)
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314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTA 373

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Search completed: August 26, 2005, 07:02:59 Job time : 220 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 26, 2005, 00:31:21 ; Search time 4629 Seconds (without alignments) 10551.492 Million cell updates/sec Run on:

1 ggagtggaatcagtgagagg.....gtaaaaaagataataagtaa 1008 US-10-724-972A-2580 1008

Title: Perfect score:

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IDENTITY NUC Gapoxt 1.0 Scoring table:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

90 ba: \*
90 htg: \*
90 low: \* GenEmbl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AR282355 Sequence AF079518 Staphyloc		DNA linear BCT 01-JAN-2003 :28, section 7 of 9 of the	228 3taphylococcus. 1,L., Lu,G., Jia,J., Tu,Y.,	Chinese National Human Genome Center at 1, Shanghai 201203, China iers						
999 6 AR282355 180 1 AF079518	ALIGNMENTS	300698 bp epidermidis ATCC 122 3. 2. 2. 2. 2.	idermidis ATCC 12 Idermidis ATCC 12 ces; Bacillales; 2698) Li,H., Fu,G., Lv nd Wen,Y.	Direct Submission Submitted (OS-NOV-2002) Chinese Nati: Shanghai, 250 Bi Bo Road, Shanghai 2 Location/Qualifiers	/organism="Staphylococcus e; /organism="Staphylococcus e; /mol_type="genomic DNA" /strain="ATCC 12228" /db_xref="ATCC:12228" /db_xref="taxon:175280"	<pre>complement(114186) /product="tRNA-Lys" complement(190264) /product="tRNA-Gln"</pre>	complement (269352) /product="tRNA-Tyr" complement (369444) /product="tRNA-Val"	complement (451522) /product="tRNA-Glu" complement (524598) /product="tRNA-Asn"	complement (612726) /product="5S ribosomal RNA" complement (8863713) /product="23S ribosomal RNA" complement (27182831) /locus tag="SE175s"	
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RESULT 2 BX571857	T 2 857_22/c		
Seg	g 8 p	into 28 fragments	LOCUS BX571857 Accession BX571857
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Mat	Matches 72	B; Conservative 0;	cches 2
δ	7	7 GAATCAGTGAGAGGTTTAAAAAT	TITAAGIGIAATIGGCITAITGITITAATIGCA 66
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ò	67	7 ACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAAGAGT	TTCAAGTAACTCAAAGAGTCATCAAAAGATGGA 126
qq	48025	s GTT	
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ò	187	7 GITCITGA	GTATTCATTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATA 246
q	47905	LO.	
غ ه	747	7 GCGGATGATAACAAAAAAAATCGTATTAATAAA	TATTATTAAACCATTAAGAGATAAAATTGGAAAATAC 306
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Kikuchi,H.

Direct Submission
Submitted (16-WAR-2002) Director-General, Biotechnology Center, Submitted (16-WAR-2002)
National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bhognite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81.3-3481-8424)
Tel:81-3-3481-1933, Fax:81.3-3481-8424)
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Sa 4mw]"
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hypothetical protein, similar to acetyltransferase
[Genomic island nu Sa 4mw]"
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hypothetical protein, similar
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/gene="MW1949"
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Director-General, Biotechnology Center, Aoki, K., Oguchi, A.,
Nagai, Y., Asano, K., Iwama, N., Baba, T., Kuroda, M., Hiramatsu, K. and
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AMPLITTEAVVASIPERKNDOPPNGGMFGMM"
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                                                                                                                                                                                                                                                                                                  truncated hypotherical protein, similar to integrase [Genomic island nu Sa 4mw]"
                              runcated hypothetical protein, similar to integrase (Genomic island nu Sa 4mw)"
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                                                                                                                                                                                                                  HTLRIAHRIRCTH"
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FLCPFILDVISFAVIPTINSQVGILLFLANGCENIILSATLKRFYEDDLKSIFYASNVLK
QGYTISKIKHAPQPRINFKQPRTAHLITSVLAEWIDBJIGAMVIKLYLLIFHLDYVLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVVPEVASRHHVEGITTTINEALVDADVSMEDIDAIAVTEGPGLIGALLIGVNAAKAL
AFAYDKPLIPVHHIAGHIYANHIEEPLTFPLIALIVSGGHTELVYMKDHLSFEVIGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein, similar to ribosomal-protein-alanine
N-acetyltransfer"
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hypothetical protein, similar to O-sialoglycoprotein
endopeptidase"
                                                                                                                                                                                                    hypothetical protein, similar to DNA mismatch repair protein Muts"
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endopeptidase"
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complement (2222. .3247)
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Birect Submission

Submitted (30-JAM-2001) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2chome 49-10 Nishibara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)

On Jun 12, 2001 this sequence version replaced gi:13701842.
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AP003136 BA000018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          847 AAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGAC
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/organism="Staphylococcus aureus subsp. aureus N315"
/mol_type="genomic DNA"
/strain="N315"
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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RATALSYARGIGATRAACHETFKERETFDLEGBQAULGGSYSKLIQSEFTLVBAGY
QPBLAYFEVLHEMKLIYDLWYBGGGENVRYGISNTAEFGDYVSGPRVTTPDVKENMKA
VLTDIQNGNFSNRFIEDNKNGFKEFYKLREEQHGHQIEKVGRELREMMPFIKSKSIEK
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'protein_id="BAB43143.1"
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10202. .11731
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/transl_table=
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TLAIANEAGI DYDLER INAIAKRTPYLSKI APSSSYSMHDVHEAGGVPAI INELMKKD
GTLHPDRITYTGKTLRENNEGKEI KWPDVI HPLAPYDAGGGLSI LEVGNIAPKGAVIK
VGGUDES I KTPTGKAI CHNSIDGKEI KWPDVI HPLAPYDAGGGLSI LEVGNIAPKGAVIK
VGGUDES I KTPTGKAI LTDGRESCALEI DNRTVRAGHVVVI RYEGPKGSPGNEBLLAP
TSSI VORGLGKDVALITDGRESCATRGI AVGHI SPEAAGGBI ALIEDGDEI TI DLIN
RTLNVNQPEDVLARRESLI PPRKAKVKTGY LARYTALVTSANTGGVMQVPENLI"
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PENKDIDT FI SLLKBAKKPVVLAGAGINOSKSOLLTNGVRWRGI PFVTTLLGLGAVP
PEDTLFLGMGGMHGSYASNMALTECDLLINGSRFDDRLASKPODAFAPNAKTLAGLASV
PEDTLFLHWGGHHGSYASNMALTECDLLINGSRFDDRLASKPODAFAPNAKTLAGLAV
VPKOTHVDLGI I ADCKRFLECLANDKNVETI EHSDWYKHCQNNKQKHPFKLGEBD
VPCKPQQT I EY I GKT TINGEA.I VTTDVGQHQWMAAQFY PFKNHGQWYTSGGLGTMGFGI
PSSTGAKLANDBKTVVCFVQDGGFQMTNQEMALLPFYGLDVKI VLINNGTLGMVKQWQ
DKFFRNORFSHSVFRQOPDFMKAAEAYCVKGFLIDKPEQLEGLDAAFPAYQGPVLI EW
I SPTEAVTPWVPSGKSNHEMEGL."
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hypothetical protein, similar to acetolactate synthase
small subunit"
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trans1 table=
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155937 TATTTGAAAGGACCTTACTTACAATTAGACACTGAACATTTAGCTGATTTAAATCCAGAG 155878

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|transl_table=11
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On Apr 16, 2004 this sequence version replaced gi:14247707.
This work was done in collaboration with Toshiko Ohta, Mutsumi
Kanamori, Hideo Hayashi (University) of Tsukuba), Hideki Hirakawa,
Satoru Kuhara (Kyushu University), Ikuo Uchiyama (Okazaki Hirakawa,
Research Institutes), Susumu Goto, Minoru Kanehisa (Kyoto
University), Naotake Ogasawara (Nara Institute of Science and
Technology) and supported by the Research for the Future Program of
the Japan Society for the Promotion of Science.
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Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.
Mateumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
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Kanahisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
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Kahabi,T., Hattori,M., Ogasawara,N., Hayashi,H., and Hiramatsu,K.
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Hattori, M., Yamashita, A., Oshima, K. and Shiba, T.
Direct Submission
Submitted (28-FEB-2001) Masahira Hattori, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara, Kanagawa 228-8555, Japon
(E-mail:hattori@genome.ls.kitasato-u.ac.jp, Tel:81-42-778-8194,
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                                           CGTATGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAA

    347650
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/strain="Mu50"

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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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DNA RESEARCH 11, 51-56 (2004)
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AP003364.3 GI:46395538
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238456 CGTGATGTTTGGGCAAGATCTCGTGGCTTAATTTCTTCTGAAGAAATGGCTAAAGAACTT 238397
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                             Length 347650;
                             Score 569; DB 1; Length 34
Pred. No. 8.3e-78;
0; Mismatches 265; Indels
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complement (7769. .8500)
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/note="Bacteriophage phi Sa 3mu"
/note="Bacteriophage phi Sa 3mu"
/codon glatat=1
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/product="hypothetical protein"
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FEPTGPYLMYNYTGYDGKGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWALDATAYKE
FRVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITKVVI
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db_xref="G1:14247717"
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/gene="truncated-lytA"
/locus tag="SAN1943"
/gene="truncated-lytA"
/locus tag="SAN1943"
/locus tag="SAN1943"
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/codon start=1
/transI_table=11
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/locus tag="SAV1942"
complement (5216. .5566)
/locus tag="SAV1942"
/note="Bacteriophage phi Sa 3mu"
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/protein_id="BAD16608.1"
/db_xref="GI:46395542"
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note="Bacteriophage phi
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complement(7063, .7554)
/gene="sak"
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/locus_tag="SAV1945"
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                                (locus_tag="SAV1941"
(617. .4925
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      "FGITACSSSIHFIN"
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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larity 73.5%; Pred. No. 2.1e-75;
Conservative 0; Mismatches 256;
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/organism="Staphylococcus /
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> AP003132 RESULT 9 AP003132 LOCUS

> > Burnham, M. K. and Hodgson, J. E. POLYNUCLEOTIDES AND AMINOACID SEQUENCES FROM STAPHYLOCOCCUS AUREUS

298050 bp

DNA

57

PAT 29-MAR-1999

linear

DNA

A64853 2247 bp Sequence 10 from Patent WO9731114.

DEFINITION

RESULT 8 A64853/c

ACCESSION VERSION

A64853 A64853.1 GI:4530844

unidentified unidentified unclassified.

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

BCT 11-JAN-2003 linear

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WKLI QPI SFPPTI SSGPI DRYKRFVKDDKKVPTGNEYRELVLKAI HMIMLGFLYKYI V
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                                                                                                                                                                                                                                                                                                                                       Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I., Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M., Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A., Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C., Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J., Sakanista,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K. Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-JAM-2001) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:blo@mite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424) On Jun 12, 2001 this sequence version replaced gi:13700734.
Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
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                                                                                                                                                                                         Staphylococcus aureus subsp. aureus N315
Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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(trans] table=11
producE="hypothetical protein"
protein_id="BAB42031.1"
db_xref="GI:13700735"
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/db_xref="taxon:158879"
280_.432
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                                        genome, section 4/10.
AP003132 BA000018
AP003132.2 GI:14349174
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/qene="SA0792"
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/gene="dltA"
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/gene="dltB"
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Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani,Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
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                                                                                                                                                                                                                                                                                  557 AAGAATATAAAAAAAAAAAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTG
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AP003361 BA000017
                                                      114080 GCAGCACTAAAAATATAACAAAGTCAGTAAGAGATAAGATTGGGGCATATGAATCGGTTG
                                                                                                                    GAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTG
                                                                                                                                                                              GATCTAGACCGCAACCGAATATGGAAGTGATAAGTAAATTAAAACCGGATTTGATTG
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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DILUVVALGFVSETFGI.EGMKDHAPQI.ENVI.TARELSRHI.EDKPANYAASKEKDDNDLS
ILVGCAGFTGVEFLGELTDRI.PELCSKYGVDQNKVKI.TCVEAAPRMLPMFSEELVNHA
                                                                                                                                                                                                               EFYALAAGTKSDKDVRNKFPNHPQVNTVYGEINDIDLDAQIVSVGNIKIDYDELIIGI
GCEDKYHNVPGAEEYTHSIOTLSKARDTFHSISELPEGAKVGIVGAGLSGIELASELR
ESSEDBLIYTYDRGPRILIRNFPEKLSKYVAKMPAKNNTVVPNSNINKVPPCKIYNCD
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APSAQLAEVQGDQIADVLKKQMLNEPLPDRMPELKVQGIVGSLGBKQGFAXIMDRTVT
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/translation="MNPIVEFCLSNMAKGGDYVFNQLENDPDVDVLEYGCLTHCGICS
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|db_xref="GI:13700145"
|translation="MAQDRKKVLVLGAGYAGLQTVTKLQKAISTEEAEITLINKNEYH
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hypothetical protein, similar to NADH dehydrogenase"
                                hypothetical protein, similar to NADH dehydrogenase" 
/codon start=1
/trans1_table=11
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Pred. No. 2.9e-32;
0; Mismatches 433; Indels
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transl_table=
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/ LTAIN LALL LOIS ** METLESGIQPSGIPTIGNY IGALKQFVDVQNDYDCYFCIVDQHA
ITMPQDRLKLRKQTRQLAAIYLASGIDPDKATLFIQSEVPAHVQAGWMLTTASVGEL
BENTQYKOKAQKAVEGIPAGLLTYPPPLMAADIVLYNTNIVPVGDDQKQHIBLTRNLVD
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ilkmyedgydeiistrskyycklyvdidslplolysiiodnpgllrrfiildnkrlo
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complement(3870. .4859)
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5153. .5548
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Yamashita,A., Oshima,K., Kuroda,M., Hattori,M., Hiramatsu,K.,
Yamashita,A., Oshima,K., Kuroda,M., Hattori,M., Hiramatsu,K.,
Kuhara,S. and Hayashi,H.
Nucleotide Substitutions in Staphylococcus aureus Strains, Mu50,
Mu3, and M315

AL DNA RESEARCH 11, 51-56 (2004)

SE Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.

S Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.

S Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.

Life Sciences, Kitasato University, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara,
Kanagawa 228-8555, Japan

(B-mall:hattoriagenome.ls.kitasato-u.ac.jp, Tel:81-42-778-8194,
Rax:81-42-778-8193)

On Apr 15, 2004 this sequence version replaced gi:14246761.
This work was done in collaboration with Toshiko Ohta, Mutamai,
Kanamori, Hideo Hayashi (University), Ikuo Uchiyama (Okazaki National
Rasearch Institutes), Susumu Goto, Minoru Kanahaa (Kyoto
University), Naotake Ogasawara (Nara Institute of Science and
Technology) and supported by the Research for the Future Program of
the Japan Society for the Promotion of Science.

Location/Qualifiers

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VPSIQAFHVNKCRFANRCNKKLDICNNQSPKMHVCEDVIVRCHLYKNEYKEI"
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Whole genome sequencing of meticillin-resistant Staphylococcus
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protein AppF homologue"
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1000. 1980
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                 AAGCTTTAGGTAAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAATTG
                                                                                                                       557 AAGAATATAAAAAAGAAATAACTATGGATAAAATCAAAAGTATTGCCTGCAGTAGGTG
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Pred. No. 8.3e-31;
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    . 975
    /organism="Staphylococcus /mol_type="unassigned DNA" /db_xref="taxon:1280"

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KTVHKYLDLAHRYTELRKELLGLDDLKMYDLYTPLIKDIKFEMPYEEAKEWHLIKALEP
WGEBYLANVYKEGLANRWYDDVENKGKRSGGYSGAHLTNPFTLLWSINTIEDLYTLVH
EPGHSAHISYFERKOPSINSDYTIFVAEVASTCNEALLSDYMDKHLDDERKLLLLNQE
LERFRATLFROTWFEAFEHKHAI EERGEPLTPTRAMEEYAKLINKYFGDSVETDEDI
SKEWSRIPHFYMNYYYQYATGYSAAQSLSHQILTECKPAVDRYINEFLKKGSSNYPI
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                                                                                                                                                                                                          /protein id="BAB57161.1"

/db xref="G114246769"

/tanslation="MLVALNEEKTRYLATTALRKTQYFCPVCGKQVILKRGLKVISHF

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HYKCRWQNSVLEPTISAMYQLQLITOGRYVYNYGYIFPEQIYIENHPIEWQLQYDLMKK

NGKSKLVNDNLNYFKLKKFIVALESKTAIIEKLINNYLNICSDRGNDVQILF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="thingt oligopeptidase homologue"
/protein_id="BAB57162.1"
/db_xref="d1:14346770"
/tb_xref="d1:14346770"

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/locus_tag="SAV1000"
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Tempelmaier, B., Fraser, C.M. and Gill, S. A method for identification, isolation and to a specific pathogen
Fatent: WO 02059148-A 301 01-AUG-2002;
Cistem Biotechnologies GmbH (AT)
Location/Qualifiers
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Organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"
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Minh, D.B., Vytvytska, O., Etz, H., Dryla, A., Weichhart, T., Hafner, M.,
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Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
Kikuchi,H.
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Submitted (06-MAR-2002) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center, 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
(E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
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Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L.,
Yamamoto,K. and Hiramatsu,K.
Genome and virulence determinants of high virulence
community-acquired MRSA
Lancet 359 (9320), 1819-1827 (2002)
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BX571857_27 2700001 2799802
Continuation [11 of 28] of BX571857 from base 1000001 (BX571857 Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 GAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTGTG
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    CAAAGTTTATGACGTTGACCGAAATAAGTGGTTGAAATCAAGGGGGATTATCGCAAGTGA
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                                                                                 915 AAGTATGGCAGAAGATTTAGAAAAAATTGCAGAAAAAG 952
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Pred. No. 3.6e-31;
0; Mismatches 437;
                                                    AGAAATGGCAAAAGAACTTGTTGAATTATCTAAGAAAG
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BX571857_18
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BX571857_01
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BX571857_11
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BX571857_2
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/codon start=1
/codon start=1
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/product="Mpochetical protein"
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/db_xr
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/protein id="BAB94664.1"
/db xref="G1:2120396"
/translation="NWHNVIIVIALIIVVISMLAMLIRVVLGPSLADRVVALDAIGLO_LMAYIALFSILLNIKYMIVVIMMIGILAFLGTAVFSKFMDKGKVIEHDQNHTD"
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/db_xref="G1:21203995"
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IVLLSNLITLTPGTvVLGVSDDRTKIYIHAIDFSTKEQEVESIKTSLEKIVREVGEI"
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PRTRAGVEPHFVWILBBAYTARPIPITAFGALLTKVGVYATARTLSHESDNVSBFSH
YVII.FLAILTIIFGCVGANYANIKKIILYNWMIAVGVILVGVAMMTSGGMIGAIYYT
LHDMLVKLALFLLIGIMIKITGTADIRQFGGLIKRYPVIGWSFFIAALSLAGIPPLSG
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GIERRRYYYYFSVLFMLIGIIGAPTTGDIPNLFVPFEVFLMSSYPLLVIGSTKIQLQE
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/db_xref="G1:21203997"
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/gene="mnhD"
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STAFFALLEASAGATLAYEDVLYPVESYLKDKNYKPYQAEVTKATNDRAKKVETNOGTYDF
DILVVALGFVSETTEI EGMEDHAFOLENVITARELSRHIEDKFRANTAASKEKDDNDLS
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VIIIIALLAMSIMSONLIPVHIAFIPIVISTENDWIMNEAMLIPSMGYIVGLLIGGTGCFPY
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VSEGFGLLQAVGKGSKHKPRLVTITYNGKDKDRAPIALVGKGITYDSGGYSIKTKNGM
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YSETRKI SDSDNYTELKPYI LI VTI VALIATFI VQTFTDSMI FGALAGVI PFE SBAYN
WYELTRK FVEGI KI MAYI GYVILTANAFRAGWANATGDI DEL VKTLTSI TGDNYLFSI I
MYYLGLI VTLGIGSERATI PEI IASLEI PFGARI GLDTWALI ALIGTASALGBSGSPA
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VEWTYDFRGERLVLADAVFYANQYQGSVIMDFNTTGAAIVALGDDKAAAFESNSKVI
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/codon start=1
/transT_table=11
                                       . .290150
organism="Staphylococcus aureus subsp. aureus MW2"
"mol_type="genomic DNA"
strain="MW2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDSTLGPTAGLNVDGQHDHIRDTCVPNFLFYNIPLMIFGTIAAMVL"
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   Location/Qualifiers
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                                                                                                                                                                                                                                                                /gene="MW0823"
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PEATURES
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BX571856_28 2800001 2902619
Continuation [11 of 29) of BX571856 from base 1000001 (BX571856 Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                          GGTTGAAATCAAGGGGATTATCGCAAGTGAAGTATGGCAGAAGATTAGAAAAAATTG 108937
                                                                                                                                              108704 Grccriarararararaaraaraacrrcccaararcaarccaaaagrrargarr 108763
                                                                                                                                                                                                                        108764 TAGCCACTGACGGAAAACGGACAAAA-----TAGAACGAAATTCATTGATCCTGCAG 108817
54194 AATTGTTTGGAGGTAAATGTGTGAATAGGAATATCGTTAAATTAGTTGTGTTTATGCTAA 54253
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                                                                        108644 regeraricaaccreaagreacaaaagacaaaacracecarerregreaacecaagegre
                                                                                                             GACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCA
                                                                                                                                                                                     TTTGGAAATCATTAAAAGCTGTGAAAGATAACAAAGTTTATGACGTTGACCGAAATAAGT
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                                     TATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTAT
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Pred. No. 7.2e-30;
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Best Local Similarity 54.3%;
Matches 539; Conservative (
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Fragment Name BES71856_00
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BX571856_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108104 AAGATGAATTAGGAACTGAAAAATTAAGAAAATCCTAAACGTGTTGTTGTATTAGAAT 108163
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complement (9275. .9616)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 ACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557 AAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 ATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 GTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCACGAAGAAGGTACTACGAAAGTACCTAAAACACCCTAAACGTGTTGTTGTTCTTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437 AACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 290150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.1%; Score 262.8; DB 1; Length Best Local Similarity 55.0%; Pred. No. 2.8e-31; Matches 541; Conservative 0; Mismatches 437; Indels
                                                                                                                                                                                                                                                                                          complement (9616. .10044)
                                                                                                                                                                                                                                                                                                                              complement (9616. .10044)
                                                                                 complement (9275. .9616)
                                                                                                                                                                                                                                                                                                                                                                     note="ORFID:MW0833"
                                                                                                                     note="ORFID:MW0832"
                                                                                                                                          codon_start=1
trans1_table=11
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1 (bases 1 to 668)
Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AAATGCATTAAGTGACGATGTAACAAAAGGTTTAAGTAAATATTTGAAAGGACCTTACTT
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                                                                                                                                                                                                                                                                                                                              TITGCTTGCTCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAA
1 (bases 1 to 668)
Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R.
Rosen,C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.1%; Score 222.6; DB 6; Length 668; 74.8%; Pred. No. 1.7e-24;
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Staphylococcus aureus polymucleotides and sequences
Patent: US 6737248-A 355 18-MAY-2004;
Location/Qualiflers
                                                             Staphylococcus aureus polynucleotides and sequences Patent: US 6593114-A 355 15-JUL-2003; Location/Qualifiers
                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                        22.1%; Score 222.6; DB 6
llarity 74.8%; Pred. No. 1.7e-24;
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/wol_type="genomic DNA"
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YfmC, YfmB; YflL; YflJ; YflI; YflH;
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                              514 GCCGAGCACAAAAAGTCATCAACGATCTAAAAGCCGAACTTCCGAAAGATGAAAACGC
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415 AATAAAATTGCTCCTACGATTGAACTGTCGATGGAGATTATAATGAAAATATT
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Sekiguchi, J.
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Homologous recombination into bacterium for the generation
polynucleotide libraries
Patent: WO 08558-A 20 20-NOV-2003;
Novozymes A/S (DK)
Location/Qualifiers
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Bacillus subtilis
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus
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Best Local Similarity 55.0%; Pred. No. 6.5e-20;
Matches 488; Conservative 0; Mismatches 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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AUTHORS
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complement (7600. 7737)
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[trans]_table=11
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Kunst, C. Ogasawara, N. Moszer I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Brans, A., Bragnell, S.C., Bronillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J. J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Pujita, M., Pujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, O., Guiseppi, G., Guy, B.J., Haga, K., Haich, J., Harwood, C.R., Hanat, A., Hilbert, H. Holasppel, S., Hosono, S., Hullo, M.F., Krain, C., Kobayashi, Y., Koetter, P., Knainer, Blanchard, M., Katin, C., Kobayashi, Y., Koetter, P., Knainer, S., Mauel, C., Medina, N., Mellado, R.D., Mizuno, M., Moestl, D., Nakai, S., Mauel, S., Mauel, C., Medina, N., Mellado, R.D., O'Reilly, M., Ogawa, K., Ogawara, A., Oudega, B., Persoctt, A.M., Persecan, E., Pujic, P., Purnelle, B., Rapport, G., Rey, M., Reynolds, S., Rieger, M., Sachie, F., Sato, T., Schleich, S., Schleich, Takabashi, H., Takabashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Tarakashi, H., Weitzenegger, T., Winters, P., Winters, P., Winters, P., Winter, E., Wohlkawa, H. F., Zumstein, R., Yoshikawa, H. F., Zumstein, R., Yoshikawa, H. B., Rayoni, S., Wohlaka, H., Bandot, H., Wamanut, R., Wam
                                                                                                                                                                                                                   GATGAGTGGAAAACGAACCCCCTCTGGAAAATCTCAAAGCGGTGAAAAATGGACAAGTC 25950
                                                                                                                                                                                                                                                                                                                                                                             25951 TATGATGCGGACCGTGACACTTGGACAAGATTCAGAGGCATCAAGTCTAGTGAAACAAGC 26010
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                                                                                                                                                                                                                                                                                                  GATATITIAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATG
775 GIGAATCCTGAGCGTATGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTA
                                                                                                                                                     835 AAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAAACGCTGTGAAAAATCAACGTGTT
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Bacillus subtilis subsp. subtilis str. 168
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 197409)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome sequence of the
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Bacillus subtilis complete genome 1011078.
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                                               GLIAGYTYNRFKOTKLPEYLGFFSGRRLVPILTAIITIILAGIFGVWPPIGSCINSF
GEWMLGLGGIGAGIFGLFNRLLIPLGHHVLANIIFWFQFGSYNGVTGDLARFFAKDPT
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FMFLSPLLYAVHAVLTGLEFTVWMLGIRSGFSFSAGAIDYVLSYGTAEKPLLLLUV
ICYAAYFIUFYVLIKALNLKTFGREDDDVDEVLDENTVQDVNENIMLKGLGGKENLO
TIDHCATRLRLTVKDTALVDEALLKKAGAKGVVKSGGQSVQVIIGPNVEFAABELRAA
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//brotecin 16="BAA22300.1"
//bb xref="G1:2443229"
//db xref="G1:24432"
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Pred. No. 4e-20;
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Matches 488; Conserv
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BRUEIDKTFWKDAVPRQVWLLPFFIDKYPVTNKOYDIFFBIEBGMILFCHPNEPQ
RKOHRRNITWDDN LIDDHPYTGIDFYDAFAYARKGKELPTEFQWEKAARGEKGNVWP
WGDKFDPAKVQYAGSLYNEPITSLKGWRENLLKAHADKELNHLTSDIFFGNGESPYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMTLLNKI QHPVAAENVFGMCI AYPNTYI RYRLI DFVEKWVPYFSAVET I INLTQDPD
DLVSPKAMDVCANHKI EBSVAYLSS I I DDVRES I SYPKKPVGLGAQKVLSTLLD I FGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPDNVGGPISDAVMNLLNEFARIPVCGAISSYNAESEADDMGPRVQSKLIKTKSLMQG
PIVSDYSDRFSECAKQLAEWLKAGKLHYEETITEGFENIPDAFLGLFKGENKGKQLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MTLLMQDHKSIYNKDIEILIEVBELITSVPENKKNDFKSLIDNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4979. .6199)
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6535. 7998
                                                                                                                                      locus_tag="BSU07450"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="GOA:034722"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="yfmg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "gene="yfmI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6397. .6468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="yfmH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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complement (3478. .4497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I PFLANSUINLI YHVENQELTRYVGDYHQFMEVYEVKKQQLEAAYKKQQQEVAELKDFV
ARNKARVSTRUMAMSRQKKLDKMDH ELAAEKPKPEHFKPRATSGKLI FETKOLVIG
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LCKLINSETNLLVLDEPTNHLDADAKEELKRALKEYKGSILLISHEPDFYMDIATETW
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TDLSGGGRTKVLLAKLLLEKPEILLLDEPTNYLDEQHIEWLKRYLQEYENAFILISHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HQYLICDQRDKYKLLQKLSRLBGMQALVFVRDIGNLSVYAEKLAYHHVBLGVLHSRAK
KMERAKIIATFEDGEFPLLLATDIAARGLDIENLPYVIHADIPDEDGYVHRSGRTGRA
GKEGNVLSLVTKLEESKLKKMAKKLGVELSEAVYAGGKLKTK"
This entry contains data from release Ri6.1 of the Subtilist database. Further data on gene annotation and detailed information about changes from previous releases can be found at http://genolist.pasteur.fr/Subtilist/.
Location/Qualifiers
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1781. 2911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCESWITKVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                  CCTGTTGGGATAGCGGATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAA
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                                                       TCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAAACACCCT
                                                                            GCCAAAGATGTGCTTAAAAAGTGTATAATAATAAGGACAAATGAGAA 11443
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Score 190.8; DB 1;
Pred. No. 2.6e-20;
0; Mismatches 357;
18.9%;
55.0%;
Query Match
Best Local Similarity 55.04
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Pred. No. 7.7e-17;
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van Sinderen,D., ten Berge,A., Hayema,B.J., Hamoen,L. and Venema,G.

Molecular cloning and sequence of comK, a gene required for genetic
competence in Bacillus subtliis

Mol. Microbiol. 11 (4), 695-703 (1994)
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Pacillus subtilisin gene (aprB) is expressed from a sigma A (sigma 43) promoter in vitro and in vivo
J. Bacteriol. 171 (5), 2657-2665 (1989)
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/note="Similarity to several hypothetical proteins, from
Haemophilus influenzae (Swiss Prot P44036), Saccharomyces
                                                                                                                                               878 IGAAAAATCAACGIGITGAIAIIIIAGACCGIGACTIAIGGGCAAGAICACGIGGIIIAA 937
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yhfr gene; yhfu gene; yhfv gene; yhtw gene; yhxo gene;
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Bacillus subtilis chromosomal DNA, region 78-80 degrees: aprE to
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1 (bases 1 to 104)
Stahl, M.L. and Ferrart, E.
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3. Bacteriol. 158 (2), 411-418 (1984)
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Noback,M.A., Terpstra,P., Holsappel,S., Venema,G. and Bron,S.
Direct Submission
Submitted (26-JUN-1997) Noback M. A., University of Groningen,
Dept. of Genetics, Kerklaan 30, Haren, 9751 NN The Netherlands
Location/Qualifiers
                                                               818 CTAACGAACCTTCACTAAAAGAACTAGAAAAAAAACTCCTGTATGGAAGAAATTAAACGCTG
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/organism="Bacillus subtilis"
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226646), and lower to many alcohol dehydrogenases."
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DYAGQNGAKCLTLQTEHHNRKARSLYEQNGYEEDTGFVHYCLNV,
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/protein id="CAA44540.1"
/db_xref="GI:2226253"
/db_xref="GOA:007616"
/db_xref="GOA:0T616"
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/db_xref="UniProt/TrEMBL:007617"
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/db_xref="GI:2226252"
/db_xref="GOA:007615"
                                                                                                                                                                       cerevisiae (Swiss Prot P39979),
/citation=[2]
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2043. .2056
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2058. .3104
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|profucin id="CAA74542.1"
|db_xref="G1:226255"
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/translation="MTAVCLVRHGETDWNLQQKCQGKTDIPLNATGERQARETGEYVK DFSWDIYVPSDFLKBLKRAKKTAEIINEYLHLPIVEMDDFKERDYGDAEGMPLEERFYKRYPD NIYPWMETLEELTDRLWGGLAKVNQAYPNKKVLIVAHGAAIHALLTEISGGDPELQST RLVNACLSNIEFBEKRRIKDYNINSHLSGFIK"
complement (3722. .3731)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding the enzyme for the first step in poly-beta hydroxybutyrate synthesis) from Chromatium vinosum (Swiss Prot P45369), Alcaligenes eutrophus (Swiss Prot P14611), Thiorystis violacea (Swiss Prot P45363), and B.subtilis (Swiss Prot P45855)."
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pddidlfeineafavkicvcsqelgippskinvrggalalghpygasgaalvtrlfye
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ERVLLACPEVESAAVVGIPDEYWGEIAVAVILGNANARTLKAMCKQKLASYKIPKKWV
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/gene="YhfU"
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/db_xref="G1:2226256"
/db_xref="G03.007619"
/db_xref="UniProt/TrEMBL:007619"
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/protein_id="CAA74544.1"
/db_xref="G1:2226257"
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Prot P22819)."
                                                                                                                                                                                                                                                                                        complement (3788. .4882)
/gene="yhf8"
                                                                                                                                                                                                                                                                                                                                                                                                 complement (3788. .4882)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (6325. .6885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="yhfs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rgianaccacciccarccreccererecresses assesses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2702 cgrecitrirgarcegaaaracaaarcaraccarrareeccaegeargaaactrcrrrac 2761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2402 AATTGACGGCTACACATCTGTCGGCACTCGCTCACAGCCAAGCATGGAAAAATCGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2762 ATCGAGACTTT -- TAACACAGGTCGGCTACCGATATGCAATCAGTACGTCAGGCAATAG
                                                                                                                                                                                                                                                                                                             agaacataaagtggcggtaacacatgarttagggaagacaaatgtgcctgagcatccgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                             2282 GCGGGTTGTTGTTCTTGAGCTAGGTTTTATTGATACACTGCTTGATCTCGGCATTACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2462 ATTAAAACCCGATTTAATTGCTGACACCCGGCATAAGAAGGTGTACGATCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2522 GAAAAAATAGCGCCGACGATTGCACTTAATAATTTAAATGCTGATTATCAGGATACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2582 reacectrocetracearrecaaaaecagreecaaecaaaeaaaaaagaaaaager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 AGAAGAACACGATAAGAAATTGAAGAATATAAAAAAAGAAATAACTATGGATAAAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                654 TGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGATGTTACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2819 CGATTCAAGCAATGGCGGCGACTCTGTGAATATGAAAATGACACTGGAGCAGCTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          774 AGTGAATCCTGAGCGTATGTTCATAATGACAAAGCAAGCTTCTAACGAACCTTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2879 AACAGATCTCGATCATCTCTCATGACAGGAAAAACAGATGACTCGACGCCGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                834 AAAAGAAC---TAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACG
                                                                                                                                                                                                                                                         117 AAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAAACACCCTAA
                                                                                                                                                                                                                                                                                                                                                                               177 ACGIGITGITGITCITGAGIATICATITGITGATGCGTTAGITGCTTTAGATGTTAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTGGGATAGCGGATGATAACAAA---AAAAATCGTATTATTAAAACCATTAAGAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 ACTTAAACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTT
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                                                                                                                            Length 12556;
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                                                                                                                                                                                          Indels
                                                                                                                               DB 1;
                                                                                                                         16.5%; Score 166.6; DB 1;
llarity 51.5%; Pred. No. 2.5e-16;
Conservative 0; Mismatches 424;
complement (6329. .6336)
/gene="yhfT"
complement (6329. .6336)
                                                                                                                                                                Similarity
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Bactilus subcilis subcess. Bacilluses. Bacillus.

I (bases i to 198743)

Kunst. F. Ogasawara.N. Moszer.I., Albertini,A.M., Alloni,G., Azevedo,V., Bertero.M.G., Bessieres.P. Bolotin.A., Borchert.S., Borriss.N. Boursier.L., Brans,A., Braun,M., Brignell,S.C., Brons,E.L., Brans,A., Braun,M., Brignell,S.C., Brons,S., Enuschi,C.V., Caldwell,B., Capuano,V., Carter,N.M. Choi,S.K., Codani,J.J., Connetton.I.F., Cummings.N.J., Daniel.R.A., Denizot.F., Devine,K.M., Dusterhoft,A., Ehrlich,S.D., Emmerson,P. T., Ebtian, K.D., Errington,J., Peuma,S., Galizzi,A., Galleron,N. Ghim,S.Y., Glaseppi,G., Guy,B.J., Haga,K., Haiser,C., Ferrari,E., Foulger,D., Fritz,C., Fujita,M., Fujita,Y., Fune,S., Galizzi,A., Gander,D., Hilbert,H., Holsappel,S., Hosono,S., Hullo,M.F., Itaya,M., Jones,L., Joris,B., Karamata,D., Kasahara,Y., Khaert-Blanchard,M., Klein,C., Kobayashi,Y., Koetter,P., Kaningstein,G., Krogh,S., Kumano,M., Mellado,R.P., Lardinois,S., Laubert,J., Lazarevic,V., Lee,S.M., Levine,A., Liu,H., Masuda,S., Mauel,C., Mediaue,C., Mediaus,N., Mellado,R.P., Mille,D., Porwollik,S., Prescott,A.M., Persecan,E., Pujic,P., Portetelle,D., Porwollik,S., Prescott,A.M., Persecan,E., Pujic,P., Rivolte,C., Schleich,S., Schroeter,R., Scoffone,F., Sako,T., Schleich,S., Schroeter,R., Scoffone,F., Sakor,T., Scorokin,A., Tanaka,T., Takahashi,H., Takemaru,K., Takeuchi,M., Tamakoshi,A., Tanaka,T., Tarpstra,P., Takenaru,K., Vaiain,A., Yamanott,R., Wannher,F., Waller,H., Waller,H., Waller,H., Waller,P., Wannher,P., Wannher,F., Wannher,F
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On Jul 7, 2003 this sequence version replaced gi:2633260.
This entry contains data from release R16.1 of the SubtiList database. Further data on gene annotation and detailed information about changes from previous releases can be found at http://genolist.pagteur.fr/SubtiList/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur, Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Bacillus subtilis subsp. subtilis str. 168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="gamma-D-glutamate-meso-diaminopimelate
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Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 focus tag="BSU09370"
function="cell wall lytic activity"
fnote="alternate gene name: cwlE, yhdD"
                                                                                                                                    Bacillus subtilis subsp. subtilis str. 168
Bacillus subtilis subsp. subtilis str. 168
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/strain="168"
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complement(38. .1504)
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complement(38. .1504)
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/transl_table=
to 1209781.
299109 AL009126
299109.2 GI:32468723
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TITLE
JOURNAL
                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
PUBMED
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                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                             AUTHORS
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TITLE

COMMENT

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LLGWAAAVLLSFLVKKIGMKLMTSDKLKKMNIVSBEGODIQMNTASQIVFILVLLVF
LPGVLSSLKISGISGPFTNMHESVLAFLPKLFAAALIVLIGMLVARLVRDIITNFLAS
IGTERFPARMGLSIYLKDTSLSAVIGTIAYVLIMIPVVISALDQLDVAGISKPAVSML
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ELSVVGMIADQIIVILLFTAAALQIVRLHFLVRIATIATATIAVLAVVILGLGLYAG
ELVRKVLASNIKGOGEKSLAPIAKYTIIALAFFMALDQLGVAATIVNSAFIIVLSGFA
LAFGLSFGLGGKDFASRYLSTFERKMQNTEIEKNRKNQNPPNDM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AHVLAHCDEPKNINCREQNTKRDMVESMAATAERIKHYEQVHGIKEVESFLDAILSIQE
HIDPSLYRPKLQMSVDDEBEEBIEBAATPYDDLMSLDEKKPKKQVKKSKKPFPPRPEKD
ILLFIEBHSRELEPWQRDILTMMREEMLYFWPQLETKIMNEGWASYWHQRIIRBLDLT
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/db_xref="G0A:P37874"
/db_xref="UniProc\Swiss-Prot:P37874"
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LAVADVFSSYLSKLPNVIIALLVLLIGWAIAKIIEKAVYKGLSKTKIDDKLFAGKKPS
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aygmptrfshwsfgkQfhkmklhydlglsklyelvInsDPCYaflldsnsllQnkllv
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/function="involved in spore cortex synthesis (stage V
muropeptidase (major autolysin) (CWBP49')"
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/db_xref="G0A:P37875"
/db_xref="UniProt/Swigs-Prot:P37875"
/db_xref="UniProt/Swigs-Prot:P37875"
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                                                                            protein_id="CAB12776.1"
db_xref="G1:2633272"
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complement(1657. .2097)
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complement(2200. .3858)
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/gene="yhdE"
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3889. .5295
/gene="spoVR"
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function="unknown"
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function="unknown"
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Kkunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
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ACTIVAAACCAGATITAATITATIGCTGATAATAATAGACACAAAGGTATITATAAAGACTT
                                         96388 GAAAAAATAGCGCCGACGATTGCACTTAATAATTAATGCTGATTATCAGGATACAAT
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0; Mismatches 50
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6593114.

    242
    /organism="unknown"
    /mol_type="genomic DNA"

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Sequence 2556 from patent US
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PRYLGAKRF
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Aagadkskgaskaiikipntrsnsgwtstdhtgeevpvyaygpgkekprglinntdga
SDEAI EPAKLNAGVVOPSKTGINPYYLGLKI PEDI EKRYNNPTEEMKKMGVQPDSGRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNITDSAAAGTALATGVKTYNNAIGVDKNGKKVKSVLEBAKQQGKSTGLVATSEINHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              locus tag="BSU09420"
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                                                                                                                       complement (5325. .6710)
                                                                                                                                                                                                                      complement (5325. .6710)
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Matches 460
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RLYIQTMEKVMANTPKVMLDGNSGNNLTVLPLEQIIKGQQTKGKSTNATSEEVRPVFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein id="AAKO2201.1"
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Pasteurellaceae; Pasteurella.
1 (bases 1 to 13792)
May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S. and
                                                                                                                                                                                                                                                                                       Zhang, O. Zhang, V. Zhang, O. Zhang, D. Zhang, M. Wang, M. Zhang, 
                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .13792
/organism="Pasteurella multocida subsp. multocida
pm70"
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Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)
21145866
Pasteurella multocida subsp. multocida str. Pm70
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transl table=11
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/gene="hflC"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                     CGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAG 327
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Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 AGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAGT
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                                                                    62 CGTATCATTAAACCAGTTAGAGAAAAATTGGGGATTATACTTCTGTAGGTAACGTAAA
                                                                                                                                           CAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTATTGCTGATAATAAT
                                                                                                                                                                           388 AGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAGT
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Patent: US 6737248-A 2556 18-MAY-2004;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 bp DNA
Sequence 2556 from patent US 6737248.
AR537994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                              /translation="wkkllitallastalaanakeitpamepsypppeltnekgeiig
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kngridvifeddtalvdmlakegslafvgdkkytnkkyfgngpgiavnkaskdliddlakglatikangeygkytydkmtk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="WRQDYRWVIAQQIPTSLLLTFVSLVVAFPLALLLFFGLSIGNKL
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TALVSLIGVEDLMRQAELVWTHQPFTWYGIAALLYLITLISQFIIRKLEFRFTRF
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51.9%; Pred. No. 8.1e-15;
tive 0; Mismatches 384;
HIIEMGDASCFINPKTEQFKQYLSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAK02210.1"
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db_xref="GI:12720338"
                                                                                                                                                                                                       protein_id="AAK02208.1"
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3233. .8904
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1904. .9587
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                                                                  PM0124"
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                                                                                                                                                                                                                          db xref="GI:1272033
                                                             /note="synonym: F
7504. .8226
/gene="art!"
                                                                                                                                     'codon start=1
'transI table=11
'product="Art1"
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trans table=11
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transl table=
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                     7504. .8226
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/gene="artQ"
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/gene="artM"
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Matches 456; Conservative
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SAFDEGTGALTYDLAAPPDLALYHAADIDVEKATALALETEGAALSYDKRIVNSEG
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AAGFWVENGEIQYPVAEITIAGQLKEMLRNIVAVGDDIEHRSNIQTGSILLEHLKVSG
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RVPHFGYADRIQEIHIKVIHILMMLIBFEMAKTE"
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Kppkayreifoyllopmled"
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/gene="hpt"
/note="aynonym: PM0121"
5424. .5963
/gene="hpt"
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5996. .6580
/gene="gmbA"
/codon Btart=1
/transl_table=11
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Ivanova, N., Sorokin, A., Anderson, I., Galleron, N., Candelon, B.,
Kaparral, V., Bhattacharyya, A., Reznik, G., Mikhailova, N.,
Lapidus, A., Chu, L., Mazur, M., Goltsman, E., Larsen, N., D'Souza, M.,
Walunas, T., Grechkin, Y., Pusch, G., Haselkorn, R., Fonstein, M.,
Ehrlich, D.S. D., Overbeek, R. and Kyrpides, N.
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Methods for monitoring multiple gene expression
Patent: WO 0229113-A 2066 11-APR-2002;
Novozymes Biotech, Inc. (US); Novozymes A/S (DR
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/mol_type="unassigned DNA"
/db_xref="taxon:1402"
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Best Local
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AX433651
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                                                                                                                                                              Jupostation 10 301332)

Ivanova, N., Sorokin, A., Anderson, I., Galleron, N., Candelon, B., Ivanova, N., Sorokin, A., Anderson, I., Galleron, N., Candelon, B., Kapatral, V., Bhattacharyya, A., Reznik, G., Mikhailova, N., D., Dapidue, A., Chu, L., Mazury, M., Goltsman, E., Larsen, N., D'Souza, M., Halunss, T., Grechkin, Y., Pusch, G., Haselkorn, R., Fonstein, M., Ehrlich, D.S. D., Overbeek, R. and Kyrpides, N. Direct Submission

Burnett Submission

Submitted (12-MAR-2003) INRA, Genetique Microbienne, Domaine de Vilvert, Jouy en Josas 78352, France

Location/Qualifiers

1. 301332
Candelon, B., Gailloux, K., Ehrlich, D.S. and Sorokin, A. The number of ribosomal RNA operons in Bacillus cereus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producE="Membrane-attached cytochrome c550" 
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complement (857, .1984)
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complement (114. .470)
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of AB017225 from base 4300001 (AE017225 Bacillus anthracis str.
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Pred. No. 5.2
                              241057 GCTGATGCAAAAGCAAAAT 241076
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/product="GTP-binding protein"
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/Gomplement (8281. . .8679)
//Ocus tag="B64298"
/Countement (8281. . .8679)
//Ccunmber="3:5.4.5"
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VYLSNLHGDVQETTVGELLFGAFLAEDLHE"
complement (870. . 9133)
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55.4%; Pred. No. 1.3e-13;
ive 0; Mismatches 241;
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/transl_table=11
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larity 55.0%; Pred. No. 5.2e-13;
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Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A.,
Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
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Nature 423 (6935), 81-86 (2003)
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Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
1. 290029
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Bacillus anthracis str. Ames section 15 of 18 of the complete
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similarity; putative"
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Direct Submission
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/locus_tag="BA4498"
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243602 CAACAACCAAACTTAGAAGAAATTAGCCGTTTAAAACCAGATTTAATTATCACAGCTTCA 243661
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                                          243542 AATAAATGGGTAAATACAAAACAAAACGAGTAAAGATGTTGTAGATGTCGGGACACGT
             AATCGTATTATTAAACCATTAAGAGATAAATTGGAAAATACACTTCTGTAGGAACACGT
                                                                             AAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAAT
                                                                                                                                            AATAGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGAT-----T
                                                                                                                                                                             243662 TTCCGTGGTAAAGCAATTAAAATGAATTAGAACAAATTGCACCAACAGTTATGTTTGAT
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AE017355_11

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RLEEAGCQVVRVAVPDERAANAIADIKKQINIPLVADIHFDYRLALKAIEGGIDKVRI
NPGNIGRRHYWBAVNAAAKERGIPIRIGVAAGSLERHILEKYGYPTADGMVEGALHHI
KILEDLDPHDIISMKASDVNLAIEAYEKARAPPYPLHLGITESGTLFAGTVKSAAG
LGAILMKGIGNTLATSLSADPVEEVKVARELLKSFGLASNAATLISCPYCGRIEIDLI
SIANEVEEYISTLQVPIKVAVLGCAVNGPGEAREADIGIAGARGEGILFRKGQVVRKV
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FKYGSFIQDSTTMVNQAIBKDLEDFKIENGELKADIBEPIQKBEGDALFVFDENTTDI
EKYONKTGLFILKDKVVSIGNGQTQTYSYNDLLGTSLEKKDLQDFISVFDSIYFULA
VIGYLVYFLQLEITTFLGITLLAPIGSAMSGQRKLSYKQVWTLTAXSYTIPTIFFMIMD
LFKIVVPGSTFIYIAVVLIVLYLIKEVPKFNEK"
                                                                                                                                                                                                                                                                                                                                                          /translation="wkrlgfflfufulgyipyydikigtlphlbhlssykktnaaqtikge
sthtkgnkerkaeketdytyktievktgetvlsiteqinkkkipsiekviddfkqlnk
stsatkiqigksykpplyq"
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/locus tag="BA4503"

complement (7513. . 7926)

/locus tag="BA4503"

/locus tag="BA4503"

/note="similar to GB:S67291, GB:S67292, GB:S67294,

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GB:M60519, GB:M60520, GB:M60521, GB:X5905, GB:X65778,

GB:X59612, SP:P05230, PID:181942, PID:182559, PID:292022,
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GB:M60520, GB:M60521, GB:X59065, GB:X65778,
SP:P05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAATTTTAAGTGTAATTGGCTTATTGTTTTGTTTTAATTGCAACTGCAGCATGTGGAAAT
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                                                                                                                                                                                                                                                                                                               product="conserved hypothetical protein"
protein_id="AAP28212.1"
db_xref="GI:30259007"
                                                             'producta"conserved hypothetical protein"
protein_id="AAP28211.1"
db_xrefa"GI:30259006"
                                                                                                                                                                                                 /locus_tag="BA4501"
5799. 6164
/locus_tag="BA4501"
/note="lafatified by Glimmer2; putative"
(trans1_table=11
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Pred. No. 4.1e-13;
0; Mismatches 243;
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product="gcpE protein"
/protein_id="AAP28213.1"
/db_xref="G1:30259008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus tag="BA4502"
note="identified by
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329. .7432
                                                table=11
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larity 55.0%;
Conservative (
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                  GB:X59612,
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Best Local S:
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Staphylococcus aureus subsp. aureus MSSA476
Bacteria, Firmicutes; Bacillales; Staphylococcus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
Barton,A., Bantley,S.D., Chillingworth,C., Cronin,A., Chillingworth,C., Chillingworth,C., Crurcher,C., Clark,L., Corton,C., Cronin,A., Doggett,J., Churcher,C., Clark,L., Corton,C., Cronin,A., Holroyd,S., Jagels,K., James,K.D., Lennard,N., Line,A., Mayes,R., Moule,S., Mungall,K., Ormond,D., Quali,M.A., Rabbinowitsch,B., Rutherford, K., Sanders,M., Sharp,S., Simmonds,M., Stevens,K., Whitehead,S., Barrell,B.G., Spratt,B.G. and Parkhill,J.
Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid usolution of virulence and drug resistance in Proc. Natl. Acad. Sci. U.S.A. 101 (26), 9786-9791 (2004)
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sippnanwinqqyabiiqailfduvgybvkphpitteelanysnnetatpkettkpst
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GKTHLMHAIGHHVLDNNPDAKVIYTSSEKFTNEFIKSIRDNEGEAFRERYRNIDVLLI
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DITPPDYETRMAILOKKIEEEKLDIPPBALNYIANQIOSNIRELEGALTRLLAYSQLL
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OIAMYLSRELTDFSLPKIGEEFGGRDHTTVIHAHEKISKOLKEDPIFKQEVENLEKEI
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'note="Ortholog of S. aureus MRSA252 (BX571856) SAR0001"
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/mol_type="genomic DNA"
/strain="MSSA476"
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Submitted (23-UUN-2004) Submitted on behalf of the Pathogen
Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, B-mail: mh3@sanger.ac.uk
Location/Qualifiers
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/locus tag="SAS0001"
/note="Pfam match to entry PF00308 bac_dnaA, Bacterial
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BK571857 2799802 bp DNA circular BC
Staphylococcus aureus strain MSSA476, complete genome.
BK571857
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                           BX571857_11
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BX571857_15
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BX571857_22
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BX571857_2
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ACCESSION
VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26493 rcagaagacriarragcacricgrericagccagraggaggaggagagacarraagaarrar 26552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 AAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAAT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGCTTTAGGTAAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAATT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26373 GAGGAGAAAAAAGAAACAAAAGCGGACAATAAAAATCAAGCTATAACAATTAAACACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCTTGAGTATTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26613 CAACAACCTAAGAAGAAATTAGCCGTTTAAAACCAGATTTAATTATCACAGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26733 CCÁTCAACAAGCAATAACGATCÁCTTTGCTGAAATGÁCAGAAACATTTAAACAAATTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AAAATITIAAGIGIAATIGGCTIAITGTITIGAATIGCAACTGCAGCATGTGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 AATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26553 AATAAATGGGTAAATACAAAACAAAACGAGTAAAGATGTTGTAGATGTCGGGACACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 AATAGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGAT-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26673 TTCCGTGGTAAAGCAATTAAAATGAATTAGAACAAATTGCACCAACAGTTATGTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 GAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                  Length 110000;
                                                                                                                                                                                                                                                                                                                                                  Score 140; DB 1; Length 110
Pred. No. 1.6e-12;
0; Mismatches 245; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragments
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Best Local Similarity 54.6%;
Matches 306; Conservative
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        200001
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  AE017355_42
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Fragment Name
BX571857 00
BX571857 01
BX571857 03
BX571857 03
BX571857 04
BX571857 06
BX571857 06
BX571857 06
BX571857 06
BX571857 06
BX571857 09
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BX571857 00/c
WPCOMMENT
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103942 TGCACCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCAAAAGT 103883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104242 AATTAAAATGCTTGTTGTTACGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA 104183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104122 GGGTACAACTGAAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCAC 104063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104002 ACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAAGAACC 103943
                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/product= DNA gyrase subunit B"
/product= DNA gyrase
/product= DNA gyrase
/product= DNA gyrase
/db xref="01:4943360"
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TVLHAGGKPGGGGGYKNGGGLHGVGGSNVNALAGOILEVYHRNETITHGAYKKGGHAGVPQFD
IKRUGTTDKTGTVIRFKADGEIFTETTVYNYTETLOGRIPPATINGOITLEBRENB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENVREDSYHYEGGIKSYVELLNENKEPIHDEPIYİHGSKDDIEVEIAIQYNSGYATNI
ITYANNI HYEGGIHEDGYRKALIRYNINSYGLSSKİKKEREKERLSGEDTREGWTAIS
IKHGDPQFEGGYKKIKAGNSYRQVUDKLINSYGLSKİKKEREKERLSGEDTREGWTAIS
VAAKKAREVTRRKSALDVASLPGKLADCSSKSPEECEIFLVEGDSAGGSTKGGRDSRY
OALDENGKILNVEKALDRILNNEI TROMITERFGTGGEDPDLAKASYKHIVYNTDA
DVDGAHIRTLLILTYFYRPRIPLIERGYYYIAQPPLYKLTOGKÇKYYYYNDRELDKLKS
ELNPTPKWSIARYKGIGEMNADQLWETTWNPEHRALLQVKLEDAIEADGYFEMLMGDV
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                                                                                                                                                                                                                                                                                                                                                                            'note="Ortholog of S. aureus MRSA252 (BX571856) SAR0005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="SAS0005"
/note="Pfam match to entry PF02518 HATPase c, Histidine
kinase-, DNA gyrase B-, and HSP90-like ATPase, score
103.9, E-value 3.4e-28"
                         /locus tag="SAS0004"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104182 TTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACATGCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 TGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCTTGAGTATTCATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 AATTITAAGTGTAATTGGCTTATTGTTTTAATTGCAACTGCAGCATGTGGAAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="SAS0005"
/note="P800154 E1-E2 ATPases phosphorylation site."
5727. .6239
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                                                                                                     /locus tag="SAS0004"
/note="PS00617 RecF protein signature 1."
                                                                                                                                                                                                                  ≖.
∾i
                                                                                                                                                                                         /locus_tag="SAS0004"
/note="PS00618 RecF protein signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.4e-10;
0; Mismatches 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 125.6;
                                                                                                                                                                                                                                                                                                                          /locus_tag="SAS0005"
/EC_number="5.99.1.3"
                                                                                                                                                                                                                                                                     10cus tag="SAS0005"
3037. .6968
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Best Local Similarity 50.9%;
Matches 413; Conservative
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/product="DNA replication and repair protein RecF"
/protein_id="CAG41776.1"
/db xref="al:49243359"
/translation="MKLNTLOLENYRNYDEVTLKCHPDVNILIGENAQGKTNLLESIY
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TLALAKSHRYSDNELLRENADYAKTEGELSYRHGYNELTMFTTKGKRQVXNHLEGS
RLTQYIGHLNYVLFAPEDLNIVKGSPQIRRRFIDMELGQISAVYLNDLAQYQRILKQK
NNYLKQLQLGQKKDLTMLSVLAQQFAEYAMKYTDKGAHFIQELESLAKPIHAGITNDK
RALSLNYLPSLKFDYAQNEAARLEETMSILSDNMQREKERGISLFGPHRDDISFDVNG
MDAQTUSGQQQQRTTALSIKLAETELMNIRVGEYPILLLDDVLSELDDSRQTHLLSTI
QHKVQTFVTTSVDGIDHEIMNNAKLYRINGGEIIK"
3912. .4526
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GVRETRRGKKLEHQDRIDIPELPEDAGSFLIIHQGEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PÜLTGVWWLIQENELICTATÖSHRLAVRKLQLEDŸSENKNVIIPGKÅLAELNKIMSDN
BEDIDIPFSASNYULFKUGNVPNTSIRLLEGHYPDYTRLPPENYBIKLSIDNGEPYHAID
RASILAREGGNNVIKASTGDDVVELSSTSPETGTVKERVDANDYEGGSLKISFNSKYM
MDALKAIDNDEVERFGTMKPFILKPKGDDSVTQLILPIRTY"
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FQTLITSGHSEFNLSGLDPDQYPLLPQVSRDDAIQLSVKVLKNVIAQTNFAVSTSETR
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/locus tags *SAS0004"
/notes *Pfam match to entry PF02463 SMC_N, RecF/RecN/SMC_N
terminal domain, score -21.4, E-value 7.5e-05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MMEFTIKRDYFITQLNDTLKAISPRTTLPILTGIKIDAKEHEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="SAS0002"
/note="Pfam match to entry PF02767 DNA_pol3_beta_2, DNA
polymerase III beta subunit, central domain, score 222.4,
E-value 7e-64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3912. .5024
/locus_tag="SAS0004"
3912. .5024
/locus_tag="SAS0004"
/note="Ortholog of S. aureus MRSA252 (BX571856) SAR0004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locus_tag="SAS0003"
note="Ortholog of S. aureus MRSA252 (BX571856) SAR0003"
                                                                                                                                                                                                                                                                                                                             note = "Ortholog of S. aureus MRSA252 (BX571856) SAR0002"
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                                                     locus tag="SAS0001"
note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_tag="SAS0002"
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polymerase III beta subunit, C-terminal domain, score
209.8, E-value 4.4e-60"
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polymerase III beta subunit, N-terminal domain, score
224.5, E-value 1.6e-64"
protein, score 681.8, E-value 3.5e-202'
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protein id="CAG41775.1"
db_xrefe="G1:49243358"
                                                                                                                                                                                                                                                                                                                                                                                                      producE="DNA polymerase III, beta chain"
protein id="CAG41774.1"
db_xref="G1:49243357"
                                                                                                                                 locus tag="SAS0001"
note="PS01008 DnaA protein signature."
                                                                                                                                                                                                               locus tag="SAS0002"
156. .3289
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3670. .3915
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EC_number="2.7.7.7"
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                             4182 TTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACATGCAAT 4123
                                                                                        1122 GGGTACAACTGAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCAC 4063
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87 TAGTICAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTIGAAATCAAGCACGAAGA 146
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                                                                                                                                                                                                                                                                                                                                                                               TITCGATGGAGATTATAAAGAAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAG
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                                                            147 AGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGTTCTTGAGTATTCATTTGT
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Staphylococcus aureus subsp. aureus MW2
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strain:NM2, section 1/10.
AP004822 BA000033
AP004822.1 GI:21203164
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nnylkglogkorthilulyaksopirrrpinsyrdnengerekiegelsilkkok
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garvottsydgidheimnaklyringgelir"
5034. 6968
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GDDQFVSTVAKVKEDAEDETNEDEQSTSTVSEDGTEQQREAVVNDETPGNAIHTEVID
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                                     Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
Kikuchi,H.
                                                                                                                                                            Direct Submission
Submitted (06-MAR-2002) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@mise.go.jp), URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
Location/Qualifiers
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gene="recF"
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Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
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                                                                                                       ACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAATGA
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Patent: US 6593114-A 604 15-JUL-2003;
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/organism="unknown"
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ARFYYLTNEGAQLERALMNYMITKHTTQHGYTEMMYPQLYNADTMYGTGQLPKREEDD
FYSKEKGEGYTTT PTAEVPLTNEYRNEI I QPGVLPEKFTGQSACFRSEAGSAGRDTRGLI
RLHQPBCVEWYRFEQDEDSWAMELEMTTNAAR I LEELGLPYRRVILCTGDIGFSASKT
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IIENEETVYGITTGFGLFSDVRIDPTQYNELQVNLIRSHACGLGEPFSKEVALVMMIL
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                                                                                                                                                                                                                    kvijyrgeekdsddvlrelinroplinloakeglalingtaamtaqgvisyiesedlgygs
Ewiaalthoslingiidayrhdvhavrnfoeqinvaarmrdwlegstlittroaeirvod
aytlrcipoihgasfqvfnyvkqolefemnaandnplifeeanetfvisggnfhgopi
                                                                                                                                                                                                                                                                               AFALDHLKUGVSELANVSERRLERLVNPQLNGDLPAFLSPEPGLQSGAMIMQYAAASL
VSENKTLAHPASVDSITSSANQEDHVSMGTTAARHGYQIIENARRVLAIECVIALQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cranslation="MLDIRLFRNEPVTVKSKIELRGDDPKVVDEILELDEQRRKLISA
TEEMKARRNKVSEEIALKKRNKENADDVIAEMRTLGDDIKEKDSQLNEIDNRMTGILC
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Pred. No. 1.9e-10;
0; Mismatches 379; Indels 20;
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                                                        /codon_start=1
fransi_table=11
/product="histidine ammonia-lyase"
/protein_id="BAB93873.1"
/db_xref="GI:2120372"
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db_xref="GI:21203173"
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/transl_table=11
/product="seryl-tRNA
                                       note="ORFID:MW0008"
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/gene="serS"
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Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and Rosen, C.A.

Stoaphylococus aureus polynucleotides and sequences

Patent: US 6737248-A 604 18-MAY-2004;

Location/Qualifiers
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   Mismatches 474;
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   460;
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LOCUS CP000001 Accession CP000001

Sequence split into 53 fragments Fragment Name Begin En CP000001\_00

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17295 AAAAAGATGGCCAAAAGGTTTTAGCTGCTTACGATAAACGTATGAAAGATTTAAAAGCTA 17236
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                                     17466 maaacgiagaaacaancecinciinaaaaccagaciinaninaioggiaacaaangcenc 17407
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272 ITATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAAC 331
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Search completed: August 26, 2005, 05:54:16 Job time : 4645 secs

156.4 149.4 143.2

ABT15032 AAZ22850 AAZ19889 ACA21545 AAV74915

ADF43555 ACC48531 AAV74549 ACA22139

(without alignments)
9265.682 Million cell updates/sec

August 25, 2005, 23:38:01 ; Search time 644 Seconds

US-10-724-972A-2580 1008

Title: Perfect score:

Sequence:

Scoring table:

Searched:

- nucleic search, using sw model

OM nucleic

Run on:

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

Copyright

ACF74610 AAH54418

ACF67367\_39 ACF65388\_08

25860 110000 110000

ACA32751 AAS71379

Aca21545 Prokaryot
Asa9530 Exaphyloc
Aca16735 Prokaryot
Aav74915 Staphyloc
Abi15032 Pathogen
Aaz22850 Staphyloc
Adf4355 Staphyloc
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ALIGNMENTS

ADS03285 standard; DNA; 1008

BP.

ADS03285;

04-NOV-2004 (first entry)

Staphylococcus epidermis polynucleotide segid 2580.

antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; computer based system; gene; ds.

Staphylococcus epidermidis.

US2004147734-A1.

29-JUL-2004.

01-DEC-2003; 2003US-00724972.

97US-0064964P. 98US-00134001. 99US-00450969. 08-NOV-1997; 13-AUG-1998; 29-NOV-1999;

(DOUC/) DOUCETTE-STAMM L. (BUSH/) BUSH D.

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Bush

Doucette-Stamm L,

WPI; 2004-580138/56. P-PSDB; ADS07057.

New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection. CCCCCXX SX X T T T T T X T X

Claim 5; SEQ ID NO 2580; 741pp; English.

The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any

1 ggagtggaatcagtgagagg......gtaaaaaagataataagtaa 1008 4390206 segs, 2959870667 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0

8780412 hits satisfying chosen parameters:

Total number of

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

geneseqn2003ds:\* geneseqn2002bs:\* geneseqn2003bs:\* geneseqn2003cs: Geneseq 16Dec04:\* geneseqn1980s:\* geneseqn2003as:\* geneseqn2001bs: genesegn1990s:\* geneseqn2001as: geneseqn2000s ; ? Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Acc48532 Staphyloc Aca19774 Prokaryot Acs4519 Staphyloc Acs1822 Staphyloc Acs1822 Staphyloc Act80398 Staphyloc Acc4837 Prokaryot Acc4837 Prokaryot Acc4854 Staphyloc Acs4854 Staphyloc Acs5481 Staphyloc Acs7415 Staphyloc Act7415 Staphyloc Act7415 Staphyloc Act7415 Staphyloc Act7415 Staphyloc Act7415 Staphyloc Act7415 Staphyloc Ads03285 Staphyloc Aca47084 Prokaryot Description ADS03285 ACA47084 ACC48532 ACA19774 AAS54519 ACF74986 AAS51822 AAT80398 ACA47237 ACC48534 AAS51612 4AT83786 AAS54387 Query Match Length DB 336.2 336.2 309.8 269.2 265.6 9 111 113 114 118 119 119 Result No.

geneseqn2004as:\*

geneseqn2004bs:

SUMMARIES

ACF74415 ABT15015

ABN92560 263.2 190.8 175. 162. 158.

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Aav74666 Staphyloc Aav76867 Staphyloc Abn92560 Staphyloc

Adf30765 Bacillus

CAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGATGTTACTAAAGGTTTA

cc given in the specification. Also described are: a recombinant expression vector, a cell comprising a recombinant expression vector of (1); c producing an S. epidermidis polypeptide; an isolated nucleic acid c producing an S. epidermidis polypeptide; an isolated nucleic acid comparising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleic acid cited above and a carrier; treating a subject for S. epidermidis infection, a recombinant or substantially composition for prevention or treatment of an S. epidermidis infection, a subject for S. epidermidis infection, a recombinant or substantially controlled to prevention or treatment of an S. epidermidis infection, a readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments a computer readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments; a computer based commercial importance a computer based system for identifying fragments of the Staphylococcus plasmids of commercial importance, a computer based system for identifying fragment of the Staphylococcus plasmids and dentifying an expression modulating fragment of the Staphylococcus genome and/or plasmids, and identifying an expression modulating fragment content on and or treatment of an Staphylococcus parewention and/or the present invention are useful for the diagnosis, infertion, This sequence and or the invention. This sequence encodes a S. epidermis protein of the invention. \$**\$**\$**\$**\$**\$** 

Sequence 1008 BP; 404 A; 129 C; 188 G; 287 T; 0 U; 0 Other;

120 240 240 300 420 420 480 480 540 9 600 999 99 9 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAA GGGATAGCGGATGATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAATTGGA **AAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAA** TITAAAACAATITCAAAAGCITTAGGTAAAGAAGAAGGAGTAAAAACGCTTAGAAGAA 541 CACGATAAGAAAATTGAAGAATATAAAAAGAAATAACTATGGATAAAAATCAAAAGGTA GGAGTGGAATCAGTGAGAGGTTTAAAAATTTTAAGTGTAATTGGCTTATTGTTTTTA ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAA GATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAAACGT GATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGT GTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAAACCTGTT GTIGTICTIGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTT CCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAA **ATTIGCTCCTACGATTIGAACTIGAAAGTTTTCGATIGAGATTATAATGAAAATATTIGATGCT** TITAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAA **CACGATAAGAAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTA** TTGCCTGCAGTAGCTGCTAAATCAGGTTTGCTTGCTCCAAGCAACTCTTATGTTGGT Gaps Query Match 100.0%; Score 1008; DB 13; Length 1008; Best Local Similarity 100.0%; Pred. No. 3.3e-175; Matches 1008; Conservative 0; Mismatches 0; Indels 0; ч 61 61 121 121 181 181 241 241 301 301 361 361 421 421 481 481 541 601 601 셤 ઠે 유 ઠે 셤 ઠે 셤 දු පු 8 8 8 g ઠે 요 કે 용 ò 셤 ò

960 960 780 840 840 900 900 the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(I a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression TTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAA ccrgagcgrargricaraargacaaacaaagcaagricraacgaaccrrcacraaaagaa CTAGAAAAAACGTCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATTT TTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAA AGTAAGTATCTTAAAAGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAAT AGTAAGTATCTTAAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAAT CCTGAGCGTATGTTCATAATGACAAACAAGCAAGTTCTAACGAACCTTCACTAAAAGAA CTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATT Zyskind JW; Xu HH; t C New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs. GAACTTGTTGAATTATCTAAGAAAGATAGTAAAAAAAGATAATAAGTAA 1008 ds; prokaryotic essential gene; cell proliferation; ĀŞ Ohlsen | Forsyth | Haselbeck R, Yamamoto R, Claim 14; SEQ ID NO 34954; 1766pp; English. #28741 Malone C, Carr GJ, BP 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342921P. 08-FEB-2002; 2002US-00722851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 ACA47084 standard; DNA; 993 gene Staphylococcus epidermidis (first entry) (ELIT-) ELITRA PHARM INC. Prokaryotic essential Zamudio C, Trawick JD, 2003-029926/02. drug design; gene. WPI; 2003-029926/ WO200277183-A2 19-JUN-2003 03-OCT-2002 Antisense; 841 , 106 ACA47084; 781 106 199 721 721 781 841 196 υ, ο, Wang g 엄 g g 셤 g ð ð ò ò 8

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cc antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway compared for cellular proliferation; (8) identifying a gene required for cellular proliferation of the biological pathway in which a proliferation-required gene or its gene product lies compared in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound acts; (9) manufacturing an antibiotic; (10) profiling the extent compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the strains is present in a culture or collection of a creating as acceptance of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational compounds and activity proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. drug disacovery programs, or for screening form part of the printed specification, but was obtained in cells requences

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Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection.
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                                                                           CCTGTATIGGAAGAATTAAACGCTGTGAAAATCAACGTGTTGATTTTAGACCGTGAC
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                                                                                                                        Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor; antibacterial; vaccine; gene; ds.
                                                                                                          TTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAAAT
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         sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, production and recovery of SRIPs. The SRIPs can be used individually, in combination, to produce anti-staphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain staphylococcal infection. They can also be used to develop diagnostic
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                                                                                               Sequence 2981 BP; 988 A; 559 C; 386 G; 1048 T; 0 U; 0 Other;
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6.8e-95;
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the following and the activity of a gene in the biological pathway to the polypeptide whose expression is inhibited to the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the activity of proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway or the agene product or that has an activity against a biological pathway or equired for proliferation, or that inhibits cellular proliferation of an identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a congound activity, (11) a culture compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (12) determining the extent compound to the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                       1028
1147 GAAGATGCAACATGGAAAAAGTTGAATGCAGTTAAAAATAATCGCGTGGATATTGTTGAC 1086
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Yamamoto R,
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Carr GJ,
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06-SEP-2001, 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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Trawick JD,
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               identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the target ftp.wipo.int/pub/published_pct_sequences
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organism. The antisense nucleic acids are useful for
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                                                                                                                                                                                                                                             Score 567; DB 8; Length 98
Pred. No. 1.5e-94;
0; Mismatches 260; Indels
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Best Local Similarity 73.6%;
Matches 723; Conservative
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes of their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia chammesly and the encoded proteins. The prokaryotes used are Escherichia coil, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coil, Staphylococcus and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the express these proteins. The proteins can antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent celectronic format directly from WiPO at the printed in celectronic format directly from WiPO at the wipo.int/pub/published_pct_sequences
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Pred. No. 8.5e-93;
); Mismatches 256;
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enzymatic assay; antibiotic target; gene; ds.
985 GTTGAATTATCAAAAAAAGAACAAAAGTAA 1014
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                     Claim 27; SEQ ID NO 4404; 511pp; English.
      23-MAY-2000; 2000US-0206849B.
26-MAY-2000; 2000US-0207727P.
23-CCT-2000; 2000US-0242578B.
27-NOV-2000; 2000US-0253625P.
22-DBC-2000; 2000US-025391P.
16-PEB-2001; 2001US-0269308P.
        2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
2000US-0253625P.
2000US-0191078P
                                                                                                      Ohlsen KL,
Xu HH;
                                                                                   (ELIT-) ELITRA PHARM INC
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                                                                                                       Haselbeck R,
                                                                                                                   Yamamoto RT,
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                                           AATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAG
                                                                                      CTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAA
                                                                                                                    TGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCAAAAG
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antibacterial; drug design.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, peudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can also be used to screen compounds in rational drug discovery programmes. The used to screen compounds in rational drug discovery programmes. The cuties acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic callular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 927 BP; 370 A; 120 C; 169 G; 268 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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21-MAR-2001; 2001WO-US009180

Staphylococcus aureus.

WO200170955-A2

27-SEP-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence encodes a novel polypeptide, which is optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Staphylococcus aureus polynucleotide and polypeptide(s) - for isolating antagonist of the polypeptide(s) useful as anti-bacterials
                                                                                                                                                                                                                                                                                                                                                                                coccus aureus WCUH 29; antagonist; antibacterial; immunogen; disease; protection; isolation; ss.
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vaccine; diseat
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expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding it, are derived from Staphylococcus aureus. Cells expressing ligands binding the polypeptide can be used to isolated candidate compounds that bind and inhibit the activity of the polypeptide. Such compounds can be used as anti-bacterial compounds. The polypeptide may also be used as an immunogen to vaccinate an animal for protection against Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                             TAATTCGTTCAACAACTTGCTAAAGCTTTAAATAAAGANAAAGAAGGCGNNAAACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         831 GGAGTGGGACNGATGAGAGTCTAAAAACTTTTAGTATATTGGGATTAATAGTTGCCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u> aagatactatttcgggtaaagatcaaaatggtacagtaaaagtrcctaaagatgcacaa</u>
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                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                 Sequence 2247 BP; 704 A; 397 C; 307 G; 802 T; 0 U; 37 Other;
                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                       Indels
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Pred. No. 2.5e-52;
0; Mismatches 229;
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ATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGATGTTACTA 712
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<u>cerareciriciarracidatacicarriceaagerrecarraneaecararacecerrana</u>
                                                                                                                                                                      CGTGTTGTTGTTCTTGAGTATTCATTTG--TTGATGCGTTAGTTGC-TTTAGATGTTAAA
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes 3 Staphylococcus aureus proteins of unknown function. The present sequence was isolated from a library of clones of the construction of riboxymes and antisense sequence can be used in the construction of riboxymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGTGGGACNGATGAGGTCTAAAAACTTTTAGTATTGGGATTAATAGTTGCCTTA 772
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                                                                                                                                                          Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - us-
isolate antimicrobial compounds, and in vaccines against S. aureus
                                                                                                                          DNA encoding 3 Staphylococcus aureus proteins of unknown function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2247 BP; 704 A; 397 C; 307 G; 802 T; 0 U; 37 Other;
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Ward JM;
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Rosenberg M,
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P-PSDB; AAW27819, AAW27821
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complement(1705.
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         AAT83786 standard; DNA; 2247 BP
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Reichard RW,
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les 580;
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The invention relates to an isolated mucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
compound a cits fragment whose expression is inhibited by the
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
compounder(5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
compound to rithat has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
compound a gene required for cellular proliferation or the biological
compound's acitivity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the extent
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compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the extent
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compound's activity; (12) identifying the target of a compound that inhibits the
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compound's criticy; (2) identifying the carginal and confection of
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                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 ATTCTATTAAAATTAAACACGAATTAGGCACAACTAAAGTTCCTAAAGATGCTAAACGTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATAGCGGATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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Xu HH;
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                                                                                                                                                        Ohlsen KL,
Forsyth RA,
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                                                                                                                                                        Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleim 14; SEQ ID NO 35107; 1766pp; English.
                                                                                                                                                        Malone C,
Carr GJ,
06-MAR-2002; 2002US-0362699P.
                                                                        (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection.
                                                                                                                                                 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA05. To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can be used individually, or production and retaphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain straphylococcal infection. They can also be used to develop diagnostic
                 AATACACTICIGIAGGAACACGIAAGCAACCIAACTIAGAAGAAATCAGIAAACTIAAAAC
                                                                                                                      422 TTGCTCCTACGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTT
                                                            CAGATTTAATTATTGCTGATAATAATAGACACACAAAGGTATTTATAAAGACTTAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                             Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor;
                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcal surface-exposed immunogenic polypeptide DNA
                                                                                                                                                                                  482 TIAAAACAATITCAAAAGCITTAGGIAAAGAAGAAGAAGGIAA 524
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983. ,1960
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                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; vaccine; gene; de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "SEIP"
                                                                                                                                                                                                                                                                                         ACC48534 standard; DNA; 2957 BP.
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                                                                                                                                                                                                                                                                           1050 TAGCAGTAGCGGGTTGTGGTCAAAAGATACTGAAGAGAAAACTGAAAATGACGACAATAA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                      1170 ATAGTTTTGCTGATTATTTAGCAGCATTAGATATGAAACCTGTTGGTATTGCAGATGATG 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1230 GCAGCACTAAAAATATAACAAAGTCAGTAAGAGATAAGATTGGGGCATATGAATCGGTTG 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1350 cagargriagcagacaraagaaaarcaaarcagaarrgagcaaaarrgcrccgacaarca 1409
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                                                                                                                                                                                                                                                                                                                     137 AGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAAACGTGTTGTTGTTCTTGAGT 196
                                                                                                                                                         17 GAGGITTAAAATTTTAAGTGTAATTGGCTTATTGTTTGTTTTAATTGCAACTGCAGCAT 76
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                                                                                                                   Gaps
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                                                                         Length 2957;
                                     Sequence 2957 BP; 1160 A; 381 C; 512 G; 904 T; 0 U; 0 Other;
                                                                       Query Match 26.7%; Score 269.2; DB 8; Length Best Local Similarity 55.4%; Pred. No. 4.6e-40; Matches 545; Conservative 0; Mismatches 433; Indels
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes their use in the discovery of movel antibiotics, the essential genes theorem and the encoded proteins. The prokaryotes used are Bacherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, conserujinosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify controller used in proliferation, to express these proteins. The proteins can antisense nucleic acids sequence is also useful to screen for homologous cubicated carried sequence encodes an essential prokaryotic of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in calcutronic format directly from WINDO at the printed pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 AATCAAGCACGAAGAAGCTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGTT 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus DNA for cellular proliferation protein #699
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26.3%; Score 265.6; DB 4; Length 9

Best Local Similarity 57.8%; Pred. No. 1.9e-39;

Matches 494; Conservative 0; Mismatches 354; Indels
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1944 CAGAAAAGCAAAATAAAATACA 1967
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26-WAY-2000; 2000US-020727P.
23-OCT-2000; 2000US-0242578P.
27-WOV-2000; 2000US-025362FP.
22-DEC-2000; 2000US-0257931P.
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Xu HH;
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P-PSDB; AAU36528.
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Yamamoto RT,
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Local Similarity
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22-DEC-2000;
16-FEB-2001;
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23-MAY-2000;
26-MAY-2000;
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Yamamoto RT,
                                    27-SEP-2001
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic of development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can entisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
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57.8%; Pred. No. 3e-35
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P-PSDB; ABM72855.
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                                                                                      The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus genes of the invention
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                                                NO 4189; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 536; Conservative
aureus, e.g. sepsis.
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allargen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the can their hyperimmune fragments are useful for the manufacture of a paramaceutical preparation, against standard in the specification, or their hyperimmune fragments are useful for the manufacture of a comprise or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; extm.reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autocimmune disease; HIV; hepatitis; gene; ds.
                                                                                                                                                                TAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAAGATCCTG
                               TAGCCACTGACGGAAAAACGGACAAAAA----TAGAACGAAATTCATTGATCCTGCAG
                                                                     TATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTAT
                                                                                         GGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAATGGCAAAAGAACTTGTTGAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pathogen specific antigen related staphylococcal DNA SEQ ID No 301
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Hafner M;
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Dryla A, Weichhart T,
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Etz H,
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3, Vytvytska
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(e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This polynucleotide sequence represents staphylococcal DNA relating to the method for identifying and producing pathogen specific antigens of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGT
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                                                                                                                                           48 ATTGTTTGTTTTAATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAA
                                                                                                                                                                   ACTAGTTGTGTTCATGCTAATTTTAGTTGTAGCAGTAGCGGGTTGTGGTCAAAAAGATAC
                                                                                                                                                                                           108 AGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAA
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                                                              T; 0 U;
                                                                                      Score 263.2; DB 8;
Pred. No. 5.4e-39;
0; Mismatches 408;
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                                                                                       vuery match 26.1%;
Best Local Similarity 55.9%;
Matches 524; Conservative 6
                                                                  Sequence 957 BP; 383 A; 116
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the following in the factor of a cell. Also included are:

the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated confidence or its fragment whose expression is inhibited by the antisense confidence or its fragment whose expression is inhibited by the confidence or its fragment whose expression is inhibited by the confidence or its fragment whose expression is inhibited by the confidence or its fragment whose expression is inhibited by the confidence or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for centure confidences the activity of the gene product or that has an activity against a blological pathway confidence or the activity of identifying a gene required for cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture compound that inhibits proliferation of an organism; or (13) identifying the target of a compound that inhibits the confidence or the strains is present in a culture or collection of convoliferation of an organism. The antisense nucleic acids are useful for for cellular proliferation or servening for homologous nucleic acids required for fearly and active compound that inhibits proliferation or the proliferation or secreening for homologous nucleic acids required for fearly active and active modelies are useful for fearly active and active modelies are useful for fearly active and active modelies are useful for fearly active and active modelies are useful for fearly active and active modelies are useful for fearly active and active modelie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antieense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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Forsyth RA,
AAGTATGGCAGAAGATTTAGAAAAATTGCAGAAAAG 952
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Yamamoto R,
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Carr GJ,
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Trawick JD,
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                                                                Length 960;
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                                                                Score 263.2; DB 8;
Pred. No. 5.4e-39;
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electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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CCTGTTGGGATAGCGGATGATAACAAAAAATCGTATTATTAAAACCATTAAGAGATAAA 294
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                            694 rigaagecrearriaarcarcecreacecreaececearaaaaacarriaraaacaeere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for generating an expression library of polynucleotides integrated by homologous recombination into the genome of a competent gram-positive bacterium host cell. The method comprises: (a) providing a non-replicating linear integration cassette; and selecting or screening for host cells that produce the polygeptides of interest. The cassette comprises: (a) a polymucleotide encoding one or polygeptides of interest; (b) a 5' flanking polynucleotide segment or upstream of the polymucleotide of (1) and comprising a first homologous region located in the 3' end of the segment; and (c) a 3' flanking polynucleotide segment downstream of the polymucleotide of (1) and comprising a second homologous region located in the 5' end of the segment. The first and second homologous regions are at least 80, 85, 90 or 1500 bp, each of which has a sequence identity of at least 80, 85, 90 or 1500 bp, each of which has a sequence identity of at least 80, 85, 90 or 95-100* with a region of the host cell integration cassette; and non-replicating inear Gram-positive host cell integration cassette; and comprising an expression library of polynucleotides integrated by homologous recombination into the genome of a competent Gram-positive becrearium host cell. The present sequence of a competent Gram-positive characterium host cell. The present sequence of a competent Gram-positive becrearium host cell. The present sequence of a competent Gram-positive characterium host cell. The present sequence of a competent dram-positive characterium host cell. The present sequence represents a Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generating an expression library of polynucleotides by introducing the linear integration cassette into the host cell and selecting or screening for host cells that produce the polypeptides of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACGTGTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 931 TCTAAGGATTCCAGAGTGATCCATGACGAAGAAGGAAAAAGGACAGTAAGCGGCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                             Bacillus subtilis strain MB1510 integration region DNA SEQ ID NO:20
                                                                                                                                                                                                                                    dB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5718 BP; 1693 A; 1089 C; 1259 G; 1677 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                expression library, Gram-positive bacterium host cell; non-replicating linear integration cassette; gene; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 357; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8; DB 12;
1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 190.8;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hansen PK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; SEQ ID NO 20; 55pp; English
                                                          ADF30765 standard; DNA; 5718 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-2002; 2002DK-0000682.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΡΙ,
                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jorgensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-012127/01.
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Best Local Similarity
                                                                                                                                                                                                                                                                            Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention.
                                                                                                                                                                                                                                                                                                                 WO2003095658-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bjornvad ME,
                                                                                                                                         12-FEB-2004
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                                                                                                   ADF30765;
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM). read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows puttative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human disease, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock for recombinant production of the polypeptides. The new DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences computer computer conditions are useful as primers or probes for isolating conditions.
/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                         Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                         Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.4%; Score 175.4; DB 2; Best Local Similarity 60.9%; Pred. No. 6e-23; Matches 227; Conservative 0; Mismatches 146;
                                                                                                                                                                                                                                                                                                                         Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1239-1240; 3271pp; English.
                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                 97EP-00100117.
                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                        96US-0009861P
                                                                                                                                                                                                                                                                                                                         Choi GH,
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.aureus vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         readable medium
                                                                                                                                                                                                 07-JAN-1997;
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                              627 TTTGCTTGCTCCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAA 686
                                                                                          triatragcacarccaaacratrcatargricgacaartriraaacgaacraggarraa 60
                                                                                                                                                       ACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAATGACAAA
                                                                                                                                                                                    121 ACAATTAGACACTGAACATTTAGCTGATTTAAATCCAGAGCGTATGATCATTATGACAGA
                                                                                                                                                                                                                    807 CAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAA
                                                                                                                                                                                                                                           181 TCATGCTAAAAAGATTCTGCTGAATTCAAGAAGTTACAAGAAGATGCAACATGGAAAA
                                                                                                                                                                                                                                                                                867 ATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATC
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of saureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 CGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide(s) and proteins derived from Staphylococcus aureus - stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 GATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 242 BP; 100 A; 31 C; 44 G; 65 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 79.3%; Pred. No. 1.5e-20;
Matches 191; Conservative 0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon PJ,
                                                                                                                                                                                                                                      Staphylococcus aureus contig SEQ ID #2556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 2272; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0009861P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97EP-00100117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                            AAV76867 standard; DNA; 242
                                361 ACAAAGTAAGGT 373
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                   toxic shock syndrome; ds.
987 TAGTAAAAAAGAT
                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.aureus vaccines.
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                                                                                                                                                                                                     16-MAR-1999
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                                                                                                                                                                AAV76867;
                                                                                         RESULT 19
                                                                                                            AAV76867
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CCGTGACTTATGGGCAAGATCACGTGGTTTAATTTTCTTCAGAAGAAATGGCAAAAGAACT
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Carr GJ,
                                                                                                                                                                                                      BP
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; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-00815242.
                                                                                                                                                                                                      ACA42836 standard; DNA; 897
                                                                                                                                                                                                                                                                             19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella multocida.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                         design; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABU38966.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200277183-A2.
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25-OCT-2001; 2
08-FEB-2002; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-2002;
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                                                                                                                                                                                                                                           ACA42836;
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Wall D,
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                                                                                                                                                                  RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epidermidis; open reading frame; ORF; bacterial infection; gene therapy; gene; ds.
                                                         CAACCTAACTTAGAAGAATCAGTAAACTTAAACCAGATTTAATTGCTGATAATAAT 387
                                                                                           181
                                                                                                                                447
                                                                                                                                                                    241
 CAGCCAAACTTAGAAAATTAGTAAAATTAAAACCGGATTTAATTATTATGCAGT
                                                                                                                                                     388 AGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Noval isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2023.
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15.7%; Score 158.2; DB 6; Length 183;
Best Local Similarity 98.2%; Pred. No. 7.7e-20;
Matches 160; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 183 BP; 73 A; 21 C; 39 G; 50 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 2023; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                     ABN92560 standard; DNA; 183 BP.
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97US-0064964P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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P-PSDB; ABP40015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial,
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08-NOV-1997;
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846 AAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGA 21 AAAAAGACCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATGTTTAGA

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the ancisted are:

(1) a vector comprising a prodiferation of a cell. Also included are:

(2) a vector comprising a prodicer operably linked to the nucleic acid cenceding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contiferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway contained for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation or the biological containing an activity against a biological pathway in which a proliferation or the test compound that inhibits gene product lies or a gene on which the test compound that inhibits are intended to product is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which the gene contiferation of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains in present in a culture or collection of containing the target of a compound that inhibits the containing proteins or screening for homologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for identifying a cidentifying the target of a compound collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for identify and the collection of an organism.
CCGTGACTTATGGGCAAGATCACGTGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                          TGTTGAATTATCTAAGAAGATAGTAAAAAAGATAATAAGTAA 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen KL,
Forsyth RA,
                                                                                                                      141 TGTTGAATTATCTAAGAAGATAGTAAAAAAGATAATAAGTAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; SEQ ID NO 30706; 1766pp; English.
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                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the twip. The sequences the proposition of the prince did not form with published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTIGITCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 GATAGCGGATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAA 302
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candidate molecules for rational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 897 BP; 293 A; 176 C; 195 G; 233 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 156.4; DB 8; Length
Pred. No. 1.8e-19;
0; Mismatches 381; Indels
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     cellular proliferation to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 51.9%;
Matches 454; Conservative
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The invention describes a method of monitoring differential expression of cases in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus cannot be a substrate containing array of Bacillus cannot cannot be a spot in the array. The method is useful for measuring the expression of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring one cannot cannot be several genes from a Bacillus cell, discovering new global expression of several genes from a Bacillus cell, discovering new cannotoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, can which Bacillus cells adapt to changes in culture conditions, can which Bacillus cells adapt to changes in culture conditions, can which Bacillus cells adapt to changes in culture conditions, can which Bacillus cells adapt to enempt on an array equals one copen or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the printed specification, but was obtained in electronic format directly from WIPO at the invention of the contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 AACGIGITGITGITCITGAGTAITCAITTGITGAIGCGITAGITGCITTAGAIGITAAAC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
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864 AGTCCAAGACTTTGTAACGAAATCCGCCAAATAA 897
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27-MAR-2001; 2001US-0279526P.
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51.8%;
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screening

New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 9415; 1766pp; English.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

'nú

Wang Wall

(ELIT-) ELITRA PHARM INC Zamudio C, Trawick JD, 2003-029926/02 P-PSDB; ABU17675

2001US-00948993. 2001US-0342923P. 2002US-00072851. 2002US-0362699P.

06-SEP-2001; 25-OCT-2001; 208-FEB-2002; 2 21-MAR-2001;

06-MAR-2002;

21-MAR-2002; 2002WO-US009107

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cancilled are:

(1) a vector comprising a promoter operably linked to the nucleic acid cancilled whose expression is inhibited by the antisense nucleic acid; (3) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding cancilleration or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a paper or tist spans product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains is or compound that inhibits the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAAAAAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferation of an organism. The ancisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 AATAGTICAAGTAACTCAAGTAAAGAGTCATCAAAAAGATGGAGTIGAAATCAAGCACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AAAATTTTAAGTGTAATTGGCTTATTGTTTTTAATTGCAACTGCAGCATGTGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAATTCTCAGTATTTTCATAGTTTTTTCTATTCGCTGTTGGATGCGGACAGCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 GAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGTTGAGTATTCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 972 BP; 405 A; 147 C; 183 G; 237 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 143.2; DB 8;
Pred. No. 4.7e-17;
0; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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55.0%;
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Matches 308; Conservative
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Antisense; ds; prokaryotic essential gene; cell proliferation;

gene #3202.

Prokaryotic essential

Bacillus anthracis design; gene

drug

03-OCT-2002

(first entry)

19-JUN-2003

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Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                TATTGCTGATAATAATAGACACAA 395
                                                                                                                                                                                                                                                                                                                                                                              CATTGCAGATGTTAGCAGACATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA16735 standard; DNA; 321 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                          12.7%;
Similarity 67.8%;
79; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200277183-A2
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drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-2003
19-JUN-2003
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Matches 179;
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Wall
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ACA16735/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia
                                                                                                                                                                       486
307 caacaaccaaactragaagaaatragccgrrraaaaccagarrraarrarcacagcrrca
                                                                                                                          AAAGCTTTAGGTAAAAGAAGAAGTAAAAAACGCTTAGAAGAACACGATAAGAAAATT
                                                                                                                                                                                                      AATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGT
                                                   AATAAATGGGTAAATACAAAACAAAACCGAGTAAAGATGTTGTAGATGTCGGGACACGT
                                                                     AAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTGCTGATAAT
                                                                                                            385 AATAGACACAAAGGTATTTATAAAGACTTAAATAAATTGCTCCTACGAT-----T
                                                                                                                                                   GAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCA
                                                                                                                                                                       427 CCATCAACAAGCAATAACGATCACTTTGCTGAAATGACAGAAACATTTAAACAATTGCA
                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus cellular proliferation inhibitory sequence #754
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                                                                                                                                                                                                                                                                                                                                                                                 prokaryotic cellular proliferation, antibiotic, drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                                                                                                   GAAGAATATAAAAAAGAAAT 575
                                                                                                                                                                                                                                                      547 GCTGATGCAAAAGCAAAAT 566
                                                                                                                                                                                                                                                                                                        ВР
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, 2000US-020727P.

, 2000US-0242578P.

, 2000US-025362P.

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, 2001US-025362P.
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                                                                                                                                                                                                                                                                                             AAS49530/c
ID AAS49530 standard; DNA; 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                        Antisense; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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26-MAY-2000;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2000;
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coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Beeudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. WIPO.int/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAAT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATAAAAGATGAATTAGGAACTGAAAAATTAAGAAAATCCTAAACGTGTTGTTGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 AATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACCCCTAAACGTGTTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAAACCTGTTGGGATAGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rcarcecaccacraaaararaacaaagrcagraagagaraagagarrcgggggggarargaarc
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prokaryotic essential gene antisense oligonucleotide #4605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 321 BP; 83 A; 73 C; 36 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 128; DB 4;
Pred. No. 2.7e-14;
0; Mismatches 85;
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16-MAR-1999 (first entry)

AAV74915;

The invention relates to an isolated muciesc acid compitising any one or the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or the fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway cequired for proliferation or that the activity against a biological pathway in which a proliferation or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibibits proliferation of an organism acts; (9) manufacturing an antibibits proliferation of an organism acts; (9) manufacturing an antibibits proliferation of an organism acts; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overaxpressed or underexpressed; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overaxpressed.

CC ompound's activity; (11) a culture comprising strains in which to brough a confideration of an organism. The attender and organism. The attender of a compound that inhibits the compound discovery programs, or consening for homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. preduired for proliferation in cells other than S. aureus, S. typhimurium antibense sequences of the invention. Note: The sequence is one of the 6213 antisanes sequences of the invention. Note: The sequence of acts for this partice of the invention of the proliferation of the printed sequences of the invention New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. The invention relates to an isolated nucleic acid comprising any Claim 1; SEQ ID NO 4605; 1766pp; English. standardise OS field) WPI; 2003-029926/02 

Sequence 321 BP; 83 A; 73 C; 36 G; 129 T; 0 U; 0 Other;

ö 251 AATCAAGCACGAAGAAGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTCT 191 271 AATAAAAGATGAATTAGGAACTGAAAAATTAAGAAAATCCTAAACGTGTTGTTGTATT 212 211 AGAATATAGTTTTTGCTGATTATTTAGCAGCATTAGATATGAAACCTGTTGGTATTGCAGA 152 TGATAACAAAAAAATCGTATTAATTAAACCATTAAGAGATAAAATTGGAAAATACACTTC 311 IGTAGGAACACGTAAGCAACCTAAGAAGAAATCAGTAAACTTAAACCAGATTTAAT 371 32 TGATGGCAGCACTAAAAATATAACAAAGTCAGTAAGAGATAAGATTGGGGCATATGAATC 92 TGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGA GGTTGGATCTAGACCGCAACCGAATATGGAAGTGATAAGTAAATTAAAACCGGATTTGAT 0; Gaps Length 321; Score 128; DB 8; Length 32 Pred. No. 2.7e-14; 0; Mismatches 85; Indels 372 TATTGCTGATAATAGACACAA 395 12.7**%**; 67.8**%**; Best Local Similarity of.o. Matches 179; Conservative Query Match Best Local Similarity 132 192 252 151 312 91 ò 유 ઠે 셤 ઠે 요 ઠે გ ઢ

carriccacarerraccacacaraa

31

AAV74915 standard; DNA; 2115 BP

RESULT 26 AAV74915 ID AAV74 XX

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9

This sequence represents one of 5191 Staphylococcus aureus DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are be used in a vaccine composition against S.aureus infection. The collypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteonyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used to recombinant production of the polypeptides can be used the accombinant production of the polypeptides or the new DNA sequences can be used for recombinant production of the polypeptides or the new DNA sequences can be used homologues of any of the S.aureus DNA sequences contained on the computer /\*tag= a /note= "these bases represent a line of missing text in /note= "these bases represent a line of missing text in the sepecification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" Computer readable medium; vaccine; S.aureus infection; immunodetection; Polynucleotide(s) and proteins derived from Staphylococcus aureus - stored on computer readable medium and used in the production of anti-S.aureus vaccines. cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection, surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds. Gaps Rosen CA; 9 Score 125.4; DB 2; Length 2115; Pred. No. 8.9e-14; 1; Mismatches 247; Indels 6; Sequence 2115 BP; 787 A; 279 C; 363 G; 622 T; 0 U; 64 Other; Fannon MR, Dillon PJ, Claim 1; Page 1535-1536; 3271pp; English. Staphylococcus aureus contig SEQ ID #604 Location/Qualifiers Barash SC, 97EP-00100117. 96US-0009861P. 12.4%; (HUMA-) HUMAN GENOME SCI INC 541. .600 Matches 289; Conservative Staphylococcus aureus. Choi GH, WPI; 1997-374922/35. Local Similarity readable medium misc\_feature 07-JAN-1997; 05-JAN-1996; EP786519-A2 30-JUL-1997 Kunsch CA, Query Match

61 AAGGCGAGAAGCGTCTGGAAAAGCATGATAAAATATTAGCGGAGATTAGAAAAATTG 120 1 ATTATAATGCAAATATTGAAGCATTTAAAACAGTCGCTAAAGCAGTAGGCAAAGAAGAAGA 458 ATTATAATGAAATATTGATGCTTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAG ሯ 셤 δ 셤

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TGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAA 937
                                                                                                                                                                                                                                                                                                                 301 argaagaacingccaanarcaarccaaagcriargaintragccachchgacgaaaaaagg 360
                                                                                                                                                                                                                                    361 ACAAAAA----TAGAACGAAATTCATTGATCCTGCAGTTTGGAAATCATTAAAAGCTG 414
                                                                                                                                                                                                                                                                                        rcaaagaraacaaagrrrargacgrrgaccgaaaraagrggrrgaaarcaagggggarra 474
                                                                                                                                                                                                                                                                                                                                            TCGCAAGTGAAAGTATGGCAGAAGATTTAGAAAAATTGCAGAAAAAGCAAAATAAAAT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; anti-HIV;
                                                                                                                                                        CTATGGATAAAATCAAAAGGTATTGCCTGCAGTAGCTGCTAAATCAGGTTTGCTTC
                       121 AACAGAGTACGTTAAAATCTGCATTTCGGTATCTCAAGAGCAGGTATGTTAATTA
                                                  ATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAA
                                                                                                     CTAACGAACCTTCACTAAAAGAACTAGAAAAAAGATCCTGTATGGAAGAAATTAAAACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pathogen specific antigen related staphylococcal DNA SEQ ID No 318
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Hafner 1
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Weichhart T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; virucide; fungicide; protozoacide;
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Dryla A,
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Minh DB, Vytvytska
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma cool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the immunity. The hyperimmune fragments are useful for the manufacture of a parameteutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament or against S. epidermidis. The manufacture of a medicament or against S. epidermidis. The antibody preparations may also against S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This conditions for the method for identifying and producing pathogen specific antigens of the 622 386 312 TGCACCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCAAAAGT 371 TTTCGATGGAGATTATAATGAAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAG 505 trcaaataaacaatcatcigataacaaagataagaaacaactrcaatraaacatgcaat 131 132 GGGTACAACTGAAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCAC 191 GCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTATTGCTGATAATAA 599 TCCGT---GCTGATCATACAAGAATTTATGCTGGTGGATATGCTGGTGAAATCTTAAATG TAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA reacerceretrateritraecretraaaceretraecretraeaarcareacaaaa 252 ACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGAATTGTAGGTCAAGAACC 372 TAGAAATGAAAAGTTTACGATCAATTATCTAAAATCGCACC------AACAG 419 TTTCTACTGATACAGTTTTCAAATTCAAAGATACAACTAAGTTAATGGGGAAAGCTTTAG GTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATATA AAAAAGA---AATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTGAAAT AAAAAGATGCAAAAGCAAAGTATAAAGATGCATGGCCATTGAAAGCTTCAGTTAACT TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA TAGACACAAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG CAGGITIGCTICCACCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTT AATTTTAAGTGTAATTGGCTTATTGTTTTTAATTGCAACTGCAGCATGTGGAAATAA AATTAAAATGCTTGTTTACGCTTGCTTTCCTACTTGTTTTTAGCAGGATGTAGTGGGAA AGGTACTACGAAAGTACCTAAAACACCCTAAAACGTGTTGTTGTTCTTGAGTATTCATTTGT TGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAA Gaps 20; Sequence 990 BP; 398 A; 141 C; 179 G; 272 T; 0 U; 0 Other; Indels Score 124; DB 8; L Pred. No. 1.5e-13; 0; Mismatches 380; Query Match
Best Local Similarity 50.7%;
Matches 412; Conservative 479 995 539 623 invention 87 72 147 267 327 387 909 12 207 192 요 g 셤 셤 ઠે g 셤 g 8 ò ò ò ò 셤 ò 셤 Š 셤 ò δ 8

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standard; DNA; 999
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methicillin, MRSA, ds.
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LUDWIG INST CANCER RES.
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and primers derived from the nucleic acid sequences may also be used detect Staphylococcus nucleic acids in a biological sample
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                                                                                       Sequence 999 BP; 402 A; 142 C; 180 G; 275 T; 0 U; 0 Other;
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Pred. No. 1.5e-13;
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TGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAA
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/product= "cbrA"
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ADF43555
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(ATCC 202108) genomic DNA including the novel cbrA gene that codes for a 310-amino acid protein (see AAY18124) of predicted mol.wt. 36.8 kDa. The sequence was obtained from overlapping clones BTACA44 and BTAGA54, which span a single operon containing the cbrA, cbrB and cbrC genes (see AAY181899-91). CbrA shows sequence homology to known genes involved in iron regulation. The invention provides 11 novel genes (see AAY1817-27). Also provided are vectors, host cells, antibodies and hybridomas. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity, and to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. Antagonists of cbrA may be useful as antibiotics to treat infections of S. aureus and other Staphylococcus spp. Also provided are novel vaccines for the prevention or attenuation of infection by staphylococcus. The isolated nucleic acid molecule is also useful for generating probes and primers, and in the recombinant production of cbrA protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AGGIACTACGAAAGTACCTAAAACACCCTAAAACGTGTTGTTGTTCTTGAGTATTCATTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGTICAAGIAACTCAAGIAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACATGCAAT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTITAAGTGTAATTGGCTTATTGTTTTAATTGCAACTGCAGCATGTGGAAATAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTAAAATGCTTGTTACGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Staphylococcus nucleic acid molecules, used to develop products for the diagnosis, prevention and treatment of Staphylococcal infections.
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                                                       CbrA gene, infection, therapy; diagnosis; vaccine; antibiotic; iron regulation; ss.
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Pred. No. 1.5e-13;
0; Mismatches 380; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 999 BP; 402 A; 142 C; 180 G; 275 T; 0 U; 0 Other;
                        Staphylococcus aureus iron regulation gene cbrA.
                                                                                                                                        Location/Qualifiers 7. .999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 24; 102pp; English.
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LUDWIG INST CANCER RES.
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50.7%;
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98US-0084674P.
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                                                                                                           Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                            Choi GH;
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01-APR-1998;
07-MAY-1998;
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Staphylococcus aureus.
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ACC48531/c
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                                                                                                                                                                                                                                                                                                              The invention describes a new isolated nucleic acid molecule comprising:
a sequence that is 95% identical to a fully defined sequence having 586-
2226 bp, or its complement; or a sequence encoding a polypeptide having a
fully defined sequence comprising 136-691 amino acids, or its complement.
The game is Staphylococcus aureus gene. The nucleic acid is useful for
preparing a vaccine against infection caused by Staphylococcus aureus.
The methods are useful for preventing or attenuating an infection caused
by a Staphylococcus, detecting Staphylococcus nucleic acids in a
biological sample obtained from an animal, and detecting Staphylococcus
antibodies in a biological sample obtained from an animal. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAAGAAAAAGCTGAAGATTTACTTAAAAAGTACGATGATAAAAGTAGCTGCATTCC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 GGGTACAACTGAAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCAC 197
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                                                                                                                                                                                                                           gene, useful for preparing a vaccine against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 999 BP; 402 A; 142 C; 180 G; 275 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encodes Staphylococcus aureus cbrA protein.
                                                                                                                                                                                                                       New Staphylococcus aureus gene, useful for
infection caused by Staphylococcus aureus.
                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 15; 61pp; English.
01-APR-1998; 98US-0080296P.
07-MAY-1998; 98US-0084674P.
18-MAX-1999; 99WO-US006199.
15-JAN-2002; 2002US-00830217.
                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                               Choi GH;
                                                                                                                                                                   2003-897737/82.
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                                                                                                                                 Simpson AJG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA02. To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antiseara. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the siderophore family of pariplasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococcal antibodies useful in staphylococcal infection. They can also be used to develop diagnostic asseays
 604
                                                                                                                                                                                        743 ACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAATGA
                                                                                                                                                                                                                           722 recaactracarcraaagaaagcarrecarraargaacgergarcararrirreragaa
545 AAAAAGATGCAAAAGCAAAGTATAAAGATGCATGGCCATTGAAAGCTTCAGTTGTTAACT
                                     CAGGITTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTT
                                                                          605 TCCGT---GCTGATCATACAAGAATTTATGCTGGTGGATATGCTGGTGAAATCTTAAATG
                                                                                                               662 ATTTAGGATTCAAACGTAATAAAGACTTACAAAAACAAGTTGATAATGGTAAAGATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surface-exposed immunogenic polypeptide; SEIP; siderophore; antibacterial; vaccine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcal surface-exposed immunogenic polypeptide DNA
                                                                                                                                                                                                                                                                  834
                                                                                                                                                                                                                                                                                               782 AATCAGATCCAAATGCGAAAGATGCTGCATTA
                                                                                                                                                                                                                                                                  803 CAAACAAAGCAAGTTCTAACGAACCTTCACTA
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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1619 TAGAAATGAAAAGTTTACGATCAATTATCTAAAATCGCACC------AACAG 1573
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                                                                                             AATTTTAAGTGTAATTGGCTTATTGTTTGTTTTAATTGCAACTGCAGCATGTGGAAATAA
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                                                                   Gaps
                                                                   20;
              Sequence 2940 BP; 955 A; 514 C; 512 G; 959 T; 0 U; 0 Other;
                                      Score 124; DB 8; Length 29
Pred. No. 1.6e-13;
0; Mismatches 380; Indels
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                                      Query Match 12.3%;
Best Local Similarity 50.7%;
Matches 412; Conservative
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SEQ ID #238.

Staphylococcus aureus contig

(first entry)

16-MAR-1999

AAV74549;

BP

AAV74549 standard; DNA; 3775

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nedium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM, Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition adminst S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of sollypeptides can also be used in a kit for the immunodetection of sollypeptides can also be used in a kit for the immunodetection of syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used for the computer of any of the S.aureus DNA sequences contained on the computer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AATTAAAATGCTTGTTACGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA
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Pred. No. 1.7e-13;
0; Mismatches 380;
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Best Local Similarity 50.7%;
Matches 412; Conservative (
                                                                                                  toxic shock syndrome; ds.
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                                                                                                                                                                  Staphylococcus aureus
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid, (2) a host cell containing the vector; (3) an isolated concluded antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding colliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for colliferation or the activity against a biological pathway required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological contains an extinity against a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent compound's activity; (11) a culture comprising strains in which the extent compound's activity; (11) a culture comprising strains in which the extent compound's activity; (11) a culture compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for for dentifying proteins or screening for homologous nucleic acids are useful for for dentifying proteins or screening for homologous nucleic acids are useful for dentifying the research manufactor acids are useful for dentifying the research and dentifying acids required for an organism. The antisense manufactor acids are useful for an extense and dentifying acids are useful for an extense and dentifying acids are useful for an acid and acids and acid and acid and acid and acid and acid and acid acid acid acid acid aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
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                                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhi
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Forsyth RA,
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0; Mismatches 158;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; SEQ ID NO 10009; 1766pp; English.
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Pred. No. 1.4
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                                                                                                                                                                      Malone C,
Carr GJ,
06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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57.6%;
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                      351 GAAAGAAAAAGAAGCTGAAGATTTACTTAAAAAGTACGATGATAAAGTAGCTGCATTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAGA---AATAACTATGGATAAAATCAAAAGGTATTGCCTGCAGTAGCTGAAATC
                 CGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAG
                                                                                                                                                                                                                                                                                                                  Trctactgatacagitticaaaticaaagatacaaciaagttaatgeggaaagcittagg
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                                                       ccgaarticgaatacataaaaatgatttaaaagatactaagattgtaggtcaagaacct
                                                                                                                                            184 GCACCTAACTTAGAGGAAATCTCTAAATTAAAACGGACTTAATTGTCGCGTCAAAAGTT
                                                                                                                                                                                                                             agaaatgaaaagrittacgatcaattatctaaatcgcacc-------aacagt
                                                                                                                                                                                                                                                                         TTCGATGGAGATTATAATGAAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAGATGCAAAAGCATATAAAGATGCATGCCATTGAAAGCTTCAGTTGTTAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGITTGCTTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTT
                                                                                                  CAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAAT
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    S. epidermidis genomic polynucleotide sequence SEQ ID NO:3782.

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                                        242 CAGTTATGTTTGATCCATCAACAAGCAATAACGATCACTTTGCTGAAATGACAGAAACAT 301
                                                                                                        302 TTAAACAAATTGCAAAAGCAGTTGGAAAAGAAGAAGAAGGTAAAAAAGTATTAGCTGATA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a muticleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused S. aureus, e.g. sepsis.
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CGAT-----TGAACTGAAAGTTTCGATGGAGATTATAATGAAATATTGATGCTT
                                                                                  482 TTAAAACAATTTCAAAAGCTTTTAGGTAAAGAAGAAGAAGGTAAAAAAACGCTTAGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 GGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCTTGAGTATTCATTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GGTACAACTGAAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target; gene; ds.
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10.9%; Score 110.2; DB 8;
Best Local Similarity 51.8%; Pred. No. 5.1e-11;
Matches 358; Conservative 0; Mismatches 313;
                                                                                                                                                                     542 ACCATAAGAAATTGAAGAATATAAAAAAAGAAT 575
                                                                                                                                                                                                           362 regaraaagcarrcecrcarecaaaagcaaaar 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the novel S. aureus genes of the invention
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                                                                                                                                                                                                                                                                                                                      ACF74610 standard; DNA; 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-120786/11.
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and (II) can have antibacterial activity and therefore can be used in vacination. The mucleic acids (I) and therefore can be used in the vacination. The mucleic acids (I) was be used to produce the S. epidemidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their creatment of S. epidermidis infections, e.g. endocarditis. AAMS3971 to AAMS5090 represent specifically claimed S. epidermidis genomic DNA polymucleotide sequences and primers which are used in the exemplification of the present invention. AAMS5091 to AAMS5090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polymucleotide sequences given in the capture of the present specification, however the sequence listing only goes up to SEQ ID NO:4445 so even though sequences are given the disclosure for SEQ ID NO:4445 to 472, no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2705 GGAGTGGAATCAGTGAGAGGTTTAAAATTTTAAGTGTAATTGGCTTATTGTTTTTA 2764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2765 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAATGTAATAAAAA 2823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAA 119
                                                     to AAH53970 represent nucleic acids (I) encoding polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGAGTGGAATCAGTGAGAGGTTTAAAAATTTTAAGTGTAATTGGCTTATTGTTTTTA
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Length 3046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3046 BP; 1103 A; 468 C; 436 G; 1039 T; 0 U; 0 Other;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.9%; Score 109.4; DB 4 Best Local Similarity 95.0%; Pred. No. 7.7e-11; Matches 113; Conservative 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R,
Yamamoto R,
                 Claim 8; Page 1413-1414; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prokaryotic essential gene #13657.
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA32000 standard; DNA; 900
                                                                                                                                                                                                                                                                                                                                                                                                                     for SEQ ID NO:4455 to 4464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacter cloacae.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       design; gene
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The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid; (2) a host cell containing the vector; (3) an isolated concising a polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for concision or the farth has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene product or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent compound's activity; (11) a culture comprising strains in which the extent compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for culturation of an organism. The antisense nucleic acids are useful for for continuar proliferation to isolate candidate molecic acids are useful. 193 316 137 AGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCTTGAGT 196 256 194 Accargeaanacecarecreseccandrecereceaecereceneanacegreereres 253 376 254 daakeeleegeekasekaakeeradaadeekireereekereraakeekaakeeraarekirid 313 CTGATAATAATAGACACAAAAGTATTTATAAAGACTTAAAATAAAATTGCTCCTACGATTG 436 AACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCAA 496 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences 134 TCTCGTTCGCCCGATGCGCTGGCCGCCGTGGACGTCAGCCCCGATCGGTATTGCCGACGATA 197 ATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATA 257 ACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAG GAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTATTG Gaps New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. ö Length 900; Sequence 900 BP; 198 A; 266 C; 256 G; 180 T; 0 U; 0 Other; 10.2%; Score 103.2; DB 8; Length 52.9%; Pred. No. 9.7e-10; artive 0; Mismatches 198; Indels NO 19870; 1766pp; Matches 222; Conservative Local Similarity SEQ ID Claim 14; 317 437 377 Query Match 셤 à ò g g ò g ò 8 셤 ò

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AAGCTTTAGGTAAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAATTG 556 AAGTGGTAGGTAAAAAAGGAGAGATGCAGGCGGTCTCGAACAACAACATAAAGAGAAGATGG 493

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WPI; 2003-029926/ P-PSDB; ABU28130.

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374 recitaAgrecegeAacgaAccaAcciaegerigAAArtriseAcreaegeGerateArcegeg

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437 AACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCAA 496
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200 Acearccecaececatrorcacearerroeceaecratraaeceorecaarcaace
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                                                                                                                                                                                                                         CTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAATAAAATTGCTCCTACGATTG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid from Photorhabdus luminescens, useful for producing insecticidal polypeptides active against Lepidoptera, and for producing insect resistant transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product "Photorhabdus luminescens insecticide protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/product= "Photorhabdus luminescens insecticide protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photorhabdus luminescens genomic DNA encoding two insecticide proteins.
                                                                                                                                   GAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCCAGATTTAATTG
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                                            ACAAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAG
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(CNRS ) CNRS CENT NAT RECH SCI.
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
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P-PSDB; ADR20889, ADR20891.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genem of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful care sensitive to P. luminescens encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                   Antibacterial, fungicide, insecticide, polymorphism, genetic analysis, detection, food, gene expression, plant, animal, microorganism, toxin, antibiotic, biopesticide, virulence factor, disease model, plague,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAAACGTGTTGTTGTTGTTGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
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9.6%; Score 96.8; DB 10; Length 90
Best Local Similarity 51.6%; Pred. No. 1.4e-08;
Matches 221; Conservative 0; Mismatches 207; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frangeul L, Kunst F,
                                                                                                                                                                                                         Photorhabdus luminescens nucleotide seguence #9357.
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                        ACF70890 standard; DNA; 909
                                                                                                                                                               20-NOV-2003 (first entry)
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Locus ACF67367 Accession Acf67367
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             from Photorhabdus luminescens which are active against insects. The proteins of the invention are toxic to Lepidoptera, specifically the genera Plutella, Heliothis, Helicoverpa, Spodoptera and Ostrinia. The DNA tanaforts sequences of the invention are useful in the preparation of transgenic, insect-resistant plants, specifically wheat and maize. The present Photorhabdus luminescens genomic DNA contains the coding sequence for the two insecticide proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 436
       invention comprises the amino acid and coding sequences of proteins
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                                                                                                                                Sequence 25860 BP; 7315 A; 5392 C; 6047 G; 7106 T; 0 U; 0 Other;
                                                                                                                                                         9.6%; Score 96.8; DB 11; Length 25860;
ilarity 51.6%; Pred. No. 1.8e-08;
Conservative 0; Mismatches 207; Indels 0;
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Continuation (9 of 13) of ACF6538B from base 800001 (Photorhabdus luminescens nucleotide WP Sequence split into 13 fragments LOCUS ACF6538B Accession Acf6538B
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Pred. No. 1.9e-08;
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Best Local Similarity 51.6%;
Matches 221; Conservative
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Search completed: August 26, 2005, 04:36:53 Job time : 653 secs

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		c 25	79.2	7.9	1353	9 CG74	3G744812
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	Converight (c) 1993 - 2005 Committed	27	79	7.8	1536	9 CL07	8538
		28	78.8	7.8	1162	9 CL07	L077122
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נית - הוסומושט	On micloic - micloic aparch mains as model	30	78.8	7.8	1217	9 CL07	8190
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	9823 037 Million cell undates/sec	c 34	78.6	7.8	181	9 CG75	3732
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scoring capie.	COLLING CADIC. TURNING TO Garbert 1.0	C 41	78.2	7.8	1277	9 AG28	AG288477
	0.1	c 42	78.2	7.8	1373	9 CG75	0869
Searched.	34239544 Bers 19032134700 residues	c 43	78.2	7.8	1453	9 AJ59	AJ591978
		44	78	7.7	722	7 CV48	CV481731

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

EST:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		_	CG757757 P053-1-D0	CL082569 CH216-167	AL226115 Tetraodon			CR734084 Tetraodon	AG429915 Mus muscu	CL461494 SAIL_1148		CF238805 AGENCOURT	CL038406 CH216-46A	AL073856 Drosophil	AG386893 Mus muscu	CL078552 CH216-151	AG278469 Mus muscu	CG745927 P039-1-A0	CL119201 ISB1-76J1		CG755650 P051-1-G0	AG332167 Mus muscu	AL229763 Tetraodon	AL108642 Drosophil
	E CI	CL674627	CF307287	CG757757	CL082569	CNS033GQ	CNS0021J	BH651171	CR734084	AG429915	CL461494	CL101048	CF238805	CL038406	CNS00HX9	AG386893	CL078552	AG278469	CG745927	CL119201	CL694436	CG755650	AG332167	CNS036A2	CNS017Y0
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40	Query Match	9.6	9.4	8.7	8.7	8.6	8.6	8.3	8.3	8.2	8.1	8.1	8.1	8.1	8.0	8.0	8.0	8.0	8.0	7.9	7.9	7.9	7.9	7.9	7.9
	Score	96.8	95.2	87.4	87.4	96.6	86.4	83.6	83.6	82.4	81.6	81.4	81.4	81.2	80.8	80.8	80.6	80.4	80.2	80	79.6	79.6	79.6	79.2	79.2
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79.2	79	79	78.8	78.8	78.8	78.8	78.8	78.6	78.6	78.4	78.4	78.4	78.4	78.2	78.2	78.2	78.2	78.2	78	78	
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## ALIGNMENTS

RESULT 1 CL674627	
٠.	CL674627 801 bp DNA linear GSS 09-JUL-2004
DEFINITION F	PRIO112C_G03_2 - PRIO112C.BK (801) MIXED SCAGE LOSMIN ILLICATY OF F. pacificus var. California Pristionchus pacificus genomic, genomic
	Burvey sequence.
ACCESSION	CL674627
U	
	Pristionchus pacificus
MSIN	Pristionchus pacificus
ш	Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
	Neodiplogasteridae; Pristionchus.
RS	Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, K.J.
TITLE	AppabB: an AcedB database for the nemacode satellite Organism
A JANATIOT.	FILECIONCHUS pariicus Nicleic Acids Res. 32 (1). D421-D422 (2004)
	Evolutionary Biology
	Max-Planck-Institute for Developmental Biology
<b>J</b>	Spemannstr. 37-39, Tuebingen D-72076, Germany
7	rel: 00497071601371
-	Fax: 00497071601498
	. od. de
	This library was generated at Caltech, Pasadena, USA and end
~	sequenced at Vancouver, Canada.
-	Seg primer: T7
•	Class: fosmid ends.
FEATURES	Location/Qualifiers
Bource	1. 801
	/organism="Pristionchus pacificus"
	/mol_type="genomic DNA"
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	4
	/clone_lib="Mixed stage tosmid_library_or_P. pacificus
	Var. Calliornia"
	/note="Vector: prplice-5 rosmid vector"
ORIGIN	
Query Match	
Best Local	Best Local Similarity 51.9%; Fred. No. 3.3e-09; Matches 21s. Consentative O. Mismatches 202: Indels O: Gaps O;
Oy 13.	137 AGCACGAAGAAGTACTACGAAAGTACCTAAACCACACACA
Db 8:	83 Aggacgaacacgcacgcrrracacrcgaaaaaacgccacaacgarrgrggrgcrggaac 142

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Conservative
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sprmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enhartoideae; Oryzae; Oryza.

Enhartoideae; Oryzae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 313 6193
Emx: 82 31 312 6355
Bmail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF307287 Linear EST 15-AUG-2003 MRNA linear EST 15-AUG-2003 HDA1--06-E11.gl OBHDAC1-overschessing transgenic rice lambda phage CDNA library I (HDA1) Oryza sativa (japonica cultivar-group) cDNA clone HDA1--06-E11, mRNA sequence.
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/mol type="nackdong"
/cultivar="Nackdong"
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/tlssue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
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phage CDNA library I (HDA1)"
                                    ATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATA
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Length 625;

Score 95.2; DB 7; Pred. No. 6.9e-09;

9.4%;

Query Match Best Local Similarity

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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J. An integrated physical and genetic map of the nematode Pristionchus
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                                                                                                                                                                         257 ACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAG
                                                                                                                                                                                                                                                                                          495 ACGATGCAAAACGCATCCTGCCCGAAGTGCGTGCGCACCTGAAACCGTGGCAGTCCGTCG
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                                           137 AGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGTTGAGT
                                                                                         615 Aggacgacacgererrracacrecanananceceacaacaacaarrargegererragaac
                                                                                                                                             197 ATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATA
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Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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Mismatches 203; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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/mol_type="genomic DNA"
/strain="California"
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Best Local Similarity
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Matches 342; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                     254 ATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
                                                                 314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAAACTTAAACCAGATTTAATTA
                                           CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAAACGCTTAGAAGAACACGATAAGAAAA
  Gaps
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  Mismatches 466; Indels
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       554 TICAAGAATATAAAAAAGAAATAACTAIGGATAAAAATCAAAAGGIATIGCCIGCAGTAG
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/organism="Xenopus tropicalis"
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="texxon:8364"
/clone="CH216-16795"
                    Genome Sequencing Center
Washington University School of Medicine
Email: submissionne@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
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High quality sequence stop: 1114.
Location/Qualifiers
Contact: Richard K Wilson
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Similarity 45.3%;
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- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and mamnoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and RST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPRC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                               TTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAG
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TIGCTGATAATAATAGACACAAAGGTATTTATAAAAGACTTAAAATAAAATTGCTCCTACGA
                                              TTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT
                                                                                                                                             CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sauzin, W. and Weissenbach, J.
Satimate of human gene number provided by genome-wide analysis using Tetracdon nigrovitidis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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/note="Genoscope sequence ID : COAG208DH12SPl~end
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46.0%; Pred. No. 3.8e-07;
tive 9; Mismatches 330; Indels
                                                                                                                                                                                                                         linear
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|mol_type="genomic DNA"
|db_xref="taxon:99883"
|clone="208P24"
                                                   974 TATCTAAGAAAGATAGTAAAAAAGATAATAAGTAA 1008
                                                                                                    Genome Res. 10 (7), 939-949 (2000)
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GSS; genome survay sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
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linkers"
BOMJP20TR BO 2 3 KB Brassica oleracea genomic clone BOMJP20,
genomic survey sequence.
BH651171
                                                                                                                                                                                                                                                                                                     1 (bases 1 to 773)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Wnpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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51.0%; Pred. No. 1.5e-06;
iive 0; Mismatches 189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359
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/strain="TO1000DH3"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                              BH651171.1 GI:18709113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il: cdtown@tigr.org
is from a doubled l
primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 197; Conservative
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CR734084/c
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                                                                                                                                                                                                                                                                                                                                                                                            180 TGTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAATAA
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                    Length 1101;
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                                       1. .1101
/organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACROSN11"
/clone lib=RPCI 98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                    44; Mismatches 447;
                                                                                                                                                                                                                                                                                    8.6%; Score 86.4; DB 9; 39.7%; Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 329; Conserv
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1362 bp DNA linear GSS 03-JUN-2004 molossinus DNA, clone: MSMg01-304L12.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriegescriken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba 350-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 GAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 AACTGAAAAGFFFCGATGGAGAFTATAATGAAATATTGATGCTTTTAAAACAATTTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82.4; DB 9; Length 1
Pred. No. 2.6e-06;
0; Mismatches 480; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus molossinus"
                                                                                                                                                                                                                                                                                                                                     Hattori,M., Toyoda,A., Noguchi,H., 1
BAC end Sequences of Library MSMg01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/sub_species="molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:57486"
/clone="MSMg01-304L12.TJ"
                           194 AAAAAATTTATATAAAAAAAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
 865 AAATTAAACGCTGTGAAAAATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                            Mus musculus molossinus
Mus musculus molossinus
                                                                                                                                                                                                       GI:48072978
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: EcoRI
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Similarity 36.2%;
                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECORI
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LIBRARY
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R.Site 1
R.Site 2
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Matches 272;
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AG429915/c
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                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACACAAAGGTATTTAT-----AAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTGCTAAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.3%; Score 83.6; DB 3; Length 1172;
47.2%; Pred. No. 1.5e-06;
iive 0; Mismatches 354; Indels 7;
                 HTC; cDNA; full-length; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                      Organism="Tetraodon nigroviridis"
|mol_type="mRNA"
|db_xref="taxon:99883"
                                                                                                                                                                                                                                                                                                http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="fish"
 GI:51232422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 47.2
23; Conservative
                                                                                                                                                                    Senoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323;
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CL101048 1017 bp DNA linear GSS 05-JAN-2004 ISB1-3604_Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-3604,
                                                                                                                                                                                                                                                                                                                               254 ATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

( (Dases 1 to 1017)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
                                                                 /db_xref="taxon:1702"
/clone="SAIL 1148 D03.v1"
/clone lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 CAAAAGCTTTAGGTAAAGAAGAAGGTAAAAAAACGCTTAGAAGAACACGATAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                              TIGAACTGAAAAGTITCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGGAACACGTAAGCAACCTAAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAATAAAATTGCTCCTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         554 TTGAAGAATATAAAAAGAAATAACTATGGATAAAAATCAAA
                                                                                                                                                                                                                                    Query Match
8.1%; Score 81.6; DB 9; 1
Best Local Similarity 54.1%; Pred. No. 3.8e-06;
Matches 185; Conservative 0; Mismatches 153;
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/organism="Xenopus tropicalis"

/mol type="genomic DNA"

/db_xref="taxon:8364"

/clone="ISB1.3604"

/clone_lib="ISB1"
'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seg primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kenopus tropicalis (western clawed frog)
                      /mol_type="genomic DNA"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 13
High quality sequence stop: 136.
Location/Qualifiers
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CL101048
CL101048.1 GI:40594683
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JOURNAL
COMMENT
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CL101048
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Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.

I (bases 1 to 1042)
S Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bavaden, J., Ko, C., Clarke, J.D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mizel, T., Kataqiri, F., Glazebrook, J., Law, M., and Goff, S.A.

A high-throughput Arabidopsis reverse genetics system

L Plant Cell 14 (12), 2985-2994 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Syngenta Biotechnology Inc.
3054 Cormwallis Rd., Research Triangle Park, NC 27709, USA
8mil: allen.sessions@syngenta.com
BMBIC Stock Number CS642250; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAIL_1148_D03.v1 SAIL Collection Arabidopsis thallana genomic clone SAIL_148_D03.v1, genomic survey sequence.
                                                                           736
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                                                                                                                        AAGAATATAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTG
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Applied Trait Genetics
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CL461494

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE PUBMED COMMENT

FEATURES

433

Gaps

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Length 1042; Indels

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LUCUSORIUS 1594 bp DNA linear GSS 31-DEC-2003 CH216-46A6 Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-46A6, genomic survey sequence.
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/clone_lib="NICHD XGC_Emb6"
/note="Vector: pGWV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
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                                                                                                                                                                                            Gaps
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                                                                                                                                                     Length 1626;
                                                                                                                                                   Score 81.4; DB 7; Length 1
Pred. No. 4.2e-06;
0; Mismatches 413; Indels
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Best Local Similarity 44.9%;
Matches 340; Conservative (
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Kenopus tropicalis (western clawed frog)

Kenopus tropicalis

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Ruharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Kenopus tro 1626;

I (bases I to 1626)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unqublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Robert M. Grainger

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAM/4680 row: g column: 21

High quality sequence stop: 316.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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AGENCOURT 15099447 NICHD_XGC_Emb6 Xenopus tropicalis cDNA clone
IMAGE:6995950 5', mRNA sequence.
                                                                                                                                                       254 ATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
                                                                                                                                                                                      314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAAACTTAAACCAGATTTAATTA
                                                                                                                                                                                                                                                                    TTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAATAAAATTGCTCCTACGA
                                                                                                                                                                                                                                                                                                                                            TIGAACTGAAAAGTTICGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis
Library Segment 1"
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                                                                               8.1%; Score 81.4; DB 9; Length 1017; 54.2%; Pred. No. 4.1e-06;
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/tissue_type="neurula"
/dev_stage="embryo, stages 14-19"
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'db xref="taxon:8364"
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Matches 188;
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JOURNAL
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                                            ORIGIN
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Unierc Summission

Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS00HX9 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR35M04 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                          292 AAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGT 351
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                                                                                                                                 854 CTGTATGGAAGAAATTAAACGCTGTGAAAATCAACGTGTTGATATTTTAGACCGTGACT
                                                                                                                                                                                                                                                            914 TATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTTGTTGAAT
      794 TCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAAGAACTAGAAAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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44.7%; Pred. No. 5.5e-06;
iive 31; Mismatches 178; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          974 TATCTAAGAAAGATAGTAAAAAAGATAATAAGTAA 1008
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey sequence. AL073856
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/clone lib="RPCI-98"
/note="end : TET3"
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
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Pred. No. 4.6e-06;
0; Mismatches 423; Indels 0;
                                                                                                                                                                                                                                                                                                                        Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Brror: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-4646"
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High quality sequence start: 471
High quality sequence stop: 522.
Location/Qualifiers
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Matches 332; Conservative
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CH216-151D21_Sp5.1 CH216 Xenopus tropicalis genomic clone
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1 (bases 1 to 1402)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                  434 TTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT
                                                                                                                                                                                                                                                                                                                                                          CTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTC
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Subdinc-orbou, Faurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-nail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the mouse BAC library MSMG01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9199

e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                AG386893 1519 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-201E07.TJ, genomic survey
                                      532 TTAGAAGAACACGATAAGAAAATTGAAGAATATAAAAAGAAATAACTATGGATAAAAAT 591
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                   TTAAATAAAATTGCTCCTACGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAAT
                                                                                                                                                           472 ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAAAGG
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BAC end Sequences of Library MSMg01
Unpublished
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/clone_lib="MSMg01 Mouse Male BAC Library"
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Mol_type="genomic DNA"

fsub_species="molossinus"

db_xref="taxon:57486"

/clone="MSMg01-201E07.TJ"
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Pred. No. 5.5e-06;
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2 (bases 1 to 1506)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                              Characteristics of the search (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriegger.riken.jp, URL:http://hgp.gsc.riken.go.jp/, 7Fe1:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTGAAGAATATAAAAAAAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAG 610
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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/clone_lib="MSMg01 Mouse Male BAC Library'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.0%; Score 80.4; DB 9; Length 1 Best Local Similarity 46.6%; Pred. No. 6.7e-06; Matches 290; Conservative 0; Mismatches 331; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
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/clone="MSMg01-048M18.T7"
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musculus molossinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 TAACTTAGAAGAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAATAGACA 392
                                                                                                                                                                                                                                                                                                              /cell line="Stock 248 F7A2, inbred N7"
/clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 TACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCTTGAGTATTCATTTGTTGATGC
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               Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp5 atctgccgtttcgatcct
Class: BAC ends
High quality sequence start: 867
High quality sequence stop: 918.
Location/Qualifiers
                                                                                                                                                                                                        'organism="Xenopus tropicalis"
                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-151D21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 AATAACTATGGATAAAAATCAAAA 596
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Contact: Richard K Wilson
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Mus musculus molossinus
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CL119201 1256 bp DNA linear GSS 05-JAN-2004 ISB1-76J12 Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-76J12, genomic survey sequence.
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Bukaryota Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Kenopus; Silurana.
I (bases i to 1256)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
Dipublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                  554 TTGAAGAATATAAAAAAGAAATAACTATGGATAAAATCAAAAGGTATTGCCTGCAGTAG
                                                                                                                                                                 734 AAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGT
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                                                        494 CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
                                                                                          614 CTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTC
                                                                                                                                                                                                                                                                         974 TATCTAAGAAGATAGTAAAAAAGATAATAAGTAA 1008
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Washington University School of Medicine
Email: submissions@wateson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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    1.256
    /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="texon:8364"
/clone="ISB1-76J12"

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High quality sequence stop: 402.
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Bukaryota, Metazoa, Nematoda; Chromadorea; Diplogasterida;
Meodiplogasteridae; Pristionchus.

1 (bases 1 to 1225)
Srinhivasan, J., Shiz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntivasan, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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 731 TTAAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTA 790
                                                                                                                                 791 TGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAAGAACTAGAAAAAG 850
                                                                                                                                                                 /db_xref="taxon:54126"
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/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
                                                                                            254 ATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA
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Max-Planck-Institute for Developmental Biology
Maya-planck-137-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
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/strain="California"
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                     851 ATCCTGTATGGAAGAATTAAA 872
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Matches 316; Conservative
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Sommer, R.J

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Matches

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POSI-1-G09.yc Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1231)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
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             Neodiplogasteridae; Pristionchus.

1 (bases 1 to 776)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of
var. California"
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Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601371
Fax: 00497071601498
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/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
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             /clone lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis
Library Segment 1"
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0
                                                                                                                                                               Score 80; DB 9; Length 1256;
Pred. No. 8e-06;
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914 TATGGGCAAGATCACGTGGTTTAAT'FTCTTCAGAAGAAATGGCAAAAGAACTTGTTGAAT 973
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BAC end Sequences of Library MSMg01
Unpublished
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-122E04.T7"
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1. .1251
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ilarity 51.0%;
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                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/db_xref="taxon:54126"
/clone lib="Ppa ECORI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
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                                                                 Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601371
Fax: 00497071601498
                            Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                     pacificus"
                                                                                                                                                 Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                    organism="Pristionchus
                                                                                                                                                                           Location/Qualifiers
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Mus musculus molossinus DNA, clone:MSMg01-122E04.T7, genomic survey
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Direct Submission
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/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 9.6e-06;
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                                                                                                                                                                                                                                                                  625 bp DNA linear GSS 01-SEP-2000 dis genome survey sequence PUC-Ori end of clone from Tetraodon nigroviridis, genomic survey
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                    434 TIGAACIGAAAAGIIITCGAIGGAGAITAIAAIGAAAAIAIIGAIGCIITIAAAACAAIII 493
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Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="215115"
/clone_lib="Genoscope sequence ID : COAG215CB08SPl-end
PUC-Ori"
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Pred. No. 1.1e-05;
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AL229763.1 GI:7888758
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Similarity 48.2%;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Ettude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 26-JUL-1999
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BACN37H18 of DrosBAC library from Drosophila melanogaster (fruit
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Drosophila melanogaster
Bukaryota; Mecazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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survey sequence T7 end of BAC
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN37H18"
/clone lib="brosbBC"
/plasmid="pBeloBAC1"
/note="end : T7"
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1 (bases 1 to 1392)
Srinhivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Srinhivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Snintegrated physical and genetic map of the nematode Pristionchus
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                                                                                                                                484 AAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACAC
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Neodiplogasteridae; Pristionchus.
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Fax: 00497071601498
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P037-3-B03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic, survey sequence.
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                 GAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTA 358
                                                                                                  AACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAATA 418
                                                                                                                                                                     AAATTGCTCCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAATATTGATG 478
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Max-Planck-Institute for Developmental Biology
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Tel: 00497071601371
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| etrain="California"
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CG744812.1 GI:37965680
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he BAC
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                                                             /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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ralf.sommer@tuebingen.mpg.de
BAC ends.
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al Similarity 44.9%;
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CL077122 1162 bp DNA linear GSS 31-DEC-2003 CH216-143E5 Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-143E5, genomic survey sequence.
CH216-151C11_Sp5.1 CH216 Xenopus tropicalis genomic clone CH216-151C11, genomic survey sequence. CL078538
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                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 1536)
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/clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
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A physical map of the xenopus tropicalis genome Unpublished (2003)
Contact: Richard K Wilson
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Similarity 51.3%; Pred. No. 1.38-05;
78; Conservative 0; Mismatches 169; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp5 atctgccgtttcgatcct
Class: BAC ends
High quality sequence start: 1061
High quality sequence stop: 1145.
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/strain="Nigerian frog"
/db_xref="taxon:8364"
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                                                                                                                                                                Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
                                                                                                                     CL078538.1 GI:40534451
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Eukaryota, Viridipantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridipantae; Streptophyta; Eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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BF273407
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                                                                                                                                                                                                                                                                    854 CTGTATGGAAGAATTAAACGCTGTGAAAATCAACGTGTTGATATTTTAGACCGTGACT 913
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/sultivar="8400"
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/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                  794 TCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATC
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/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
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100 Jordan Hall, Clemson, SC 29634, USA 161 064 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATAGGCTCACTATAGGG
High quality sequence start: 540
High quality sequence stop: 1175.
Location/Qualifiers
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    .1185
/organism="Gossypium arboreum"
/mol_type="mRNA"

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                                                                                                                                                         Xenopus tropicalis
Ambaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodine; Xenopus; Silurana.
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/clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                   X Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R. Mardis, E. and Wilson, R. A physical map of the xenopus tropicalis genome Unpublished (2003)

Contact: Richard K Wilson Genome Sequence Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu Insert Longth: 17500 Std Error: 0.00 Seq primer: Sp6 ATTAGGTGACACTATAG Class: BAC ends High quality sequence step: 808.

I. :165 ATTAGGTGACACTATAG Class: Location/Qualifiers

I. :165 ATTAGGTGACACTATAG Class: Molity sequence step: 808.

I. :166 ATTAGGTGACACTATAG Class: Molity sequence step: 808.

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                                                                                                                          Xenopus tropicalis (western clawed frog)
                                           GI:40533035
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I (Dases 1 to 1217)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardia,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

L Unpublished (2003)

Contact: Richard K Wilson

Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wateon.wastl.edu
Insert Length: 175000
Seg primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 229
High quality sequence stop: 312.
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            434 TIGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT
                                                         CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
                                                                                                         734 AAGGACCTTACTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="caxon:8164"
/clone="CH216-148G2"
=
                                                                                                                                                                                                                                                                                                                                                                           CTGTATGGAAGAATTAAACGCTGTGAAAAATCAA
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                           854
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CL078190/c
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UG/24010 1276 bp DNA linear GSS 24-OCT-2003 P049-2-C03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
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/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTCATAATGACAAAGCAAGTTCTAACGAACCTTC----ACTAAAAGAACTAG
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Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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9
                                                                   Score 78.8; DB 9; Length 1
Pred. No. 1.4e-05;
0; Mismatches 412; Indels
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                                                                        7.8%;
                                                                          Query Match 7.8%
Best Local Similarity 45.0%
Matches 342, Conservative
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Hattori, M., Toyoda, A., Noguchi, H., 1
BAC end Sequences of Library MSMg01
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/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MSMg01-146K03.TJ"
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1. .1472
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                     Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 78.8; DB 9; Length 1276;
Pred. No. 1.4e-05;
0; Mismatches 450; Indels 0;
                                                                                                                                                                                                    Contact: Sommer RJ
Evolutionary Blology
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Email: ralf.sommer@tuebingen.mpg.de
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'strain="California"
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Best Local Similarity 40.4%;
Matches 305; Conservative
  (bases 1 to 1276)
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gesc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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Mus musculus molossinus DNA, clone:MSMg01-146K03.TJ, genomic survey
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914 TATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTTGTTGAAT 973
                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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/clone_lib="MSMg01 Mouse Male BAC Library"
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organism="Gallus gallus"
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

(kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.

(anlus gallus BAC End Reads
Unpublished (2003)
                                                                         554 TIGAAGAATATAAAAAAAAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAG
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TTGAACTGAAAGTTTCGATGGAGATTATAAAGAAAATATTGATGTTTTAAAACAATTT
                                                                                                   CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 19
High quality sequence stor: 132.
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CH261-67F12_Sp6.1 CH261 Gallus g
genomic survey sequence.
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                                                                                            /cell_line="UCD001, inbred 256"
/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoCR56 Female_CH6ken library - for library and clone CH261 Female_library - the library and clone ordering information: http://www.chori.org/bacpac"
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llarity 40.5%; Pred. No. 1.5e-05;
Conservative 0; Mismatches 449;
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/strain="Red_Jungle_Fowl"
/db_xref="taxon:9031"
/clone="CH561-67F12"
/sex="female"
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
CG753732 1811 bp DNA linear GSS 24-OCT-2003 P048-4-G03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
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/clone_lib="Ppa RooRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGGTAAGAAAA
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Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.8%; Score 78.6; DB 9; Length 1811;
llarity 37.4%; Pred. No. 1.5e-05;
Conservative 0; Mismatches 473; Indels 0
                                                                                                                                                                                                                                                                                               Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                                    Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                                 Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers,
                                                              CG753732.1 GI:37978509
                                                                                             Pristionchus pacificus
                                                                                                                                                                                                                                                                                    Contact: Sommer RJ
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Matches 282;
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1 (bases 1 to 116)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,B. and Wilson,R.
A physical map of the xenopus tropicalis genome (Unpublished (2003)
                                                                                                                                            CTGTATGGAAGAAATTAAACGCTGTGAAAATCAACGTGTTGATATTTTAGACCGTGACT 913
                                                                                                                                                                                                                                            AAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGT 793
                                          /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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CH216-161H3 RM4.1 CH216 Xenopus tropicalis genomic clone
CH216-161H3, genomic survey sequence.
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Best Local Similarity 44.0%; Pred. No. 1.7e-05;
Matches 331; Conservative 0; Mismatches 422; Indels
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM4 ctcaagggcatcggtcgagc
Class: BAC ends
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/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-161H3"
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High quality sequence stop: 926.
Location/Qualifiers
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                                           1. .1297
/organism="Pristionchus pacificus"
/ordanism="Pristionchus pacificus"
/ordanism="california"
/db_xref="taxon:54126"
/db_xref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
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                                                                                                                                                                                                     Length 1297
                                                                                                                                                                                                  7.8%; Score 78.4; DB 9; Length 1 larity 40.7%; Pred. No. 1.7e-05; Conservative 0; Mismatches 448; Indels
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                            Location/Qualifiers
                BAC ends
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ses 307; Conserv
 Email:
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Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea; Diplogasterida;
Bukaryota, Metazoa, Nematoda, Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

1 (Dases 1 to 1297)
Sriniuvasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1297 bp DNA linear GSS 24-OCT-2003
BAC Library Pristionchus pacificus genomic,
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   GAAGAATATAAAAAAAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCT
                               GAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAAACAATTTCA
                                                                                                                   AAAGCTTTAGGTAAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAATT
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                                                                                                                                                                                                                                                                                             856 GTATGGAAGAATTAAACGCTGTGAAAATCAACGTGTTGATATTTTAGACCGTGACTTA
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Max-Planck-Institute for Developmental Biology
Spenanustr. 37-39, Tuebingen D-72076, Germany
Tax: 00497071601371
Fax: 00497071601498
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P053-3-811.zb Ppa EcoRI
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CG758143/c
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CG744815
1380 bp DNA linear GSS 24-OCT-2003
P037-3-B04.za Ppa BCORI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
CG744815.1 GI:37965683
                                                                                                                                              1 (bases 1 to 1380)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:54126"
/clone ltb="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
/note="The library was generated by a partial digest
ector."
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                                                                                      Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 78.4; DB 9; Length 1380; 40.4%; Pred. No. 1.7e-05; ive 0; Mismatches 378; Indels 0
                                                                                                                                                                                                                                                                                   Evolutionary Biology
Max-Planck-Innetitute for Developmental Biology
Remannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                    Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1380
/organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                           Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                   mol type="genomic DNA"
strain="California"
                                                                                                                                                                                                                                                                                                                                               Fax: 00497071601498
                                                                                                                                                                                                                                                                      Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 40.4 Matches 256; Conservative
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1373
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                                                                                                          853
AAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGT 793
                                                   Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibla, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
I (bases I to 1594)
Iremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A pysaical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="ISB1-53P23"
/clone lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
                                                                                                             794 TCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 ATGATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTT
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46.2%; Pred. No. 1.7e-05;
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Mashington University School of Medicine
Email: submissions@wateon.wuefl.edu
Insert Length: 75000 Std Brror: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                                                                                        854 CTGTATGGAAGAATTAAACGCTGTGAAAAATCA 887

    1594
    ^organism="Xenopus tropicalis"
    ^mol_type="genomic DNA"
    ^db_xref="taxon:8364"

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CL037168 11-DEC-2003 11-DEC-2003 1-DEC-2003 CH216-42N18 Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-42N18, genomic survey sequence.
                                                                                                                                                                                                   TTAAATAAAATTGCTCCTACGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAAT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAAGG 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 TTAGAAGAACACGATAAGAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAAT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Acnopodinae; Xenopus; Silurana.

1 (bases 1 to 1110)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                           AAACTTAAACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 ccircecroridaecroccirracciraariacressirroccessarirririr
                                                                                                                                                        232 AAACCTGTTGGGATAGCGGATGATAACAAAAAAATCGTATTAATAAACCATTAAGAGAT
                                                                                                                                                                                                                                                292 AAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGT
                                                                172 CCTAAACGTGTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTAGATGTT
                   Indels
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/cell line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
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Washington University School of Medicine
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Pred. No. 1.8e-05;
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/mol_type="genomic DNA"
/strain="Nigerian frog"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: submissions@watson.wustl.edu
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High quality sequence stop: 150.
Location/Qualifiers
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/clone="CH216-42N18"
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CL037168.1 GI:40491901
  Best Local Similarity 42.1%;
Matches 179; Conservative
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CL037168/c
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AGENCOURT_14304648 NIH_MGC_173 Homo sapiens CDNA 5', mRNA sequence.
CD388253
  /tissue_type="embryonic trophoblasts, made from WA01 stem
                                                                       610
                                                                                                                                                                                                                                                            731 TTAAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                             791 TGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-WGC http://mgc.nci.nih.gov/.

NIH-WGC http://mgc.nci.nih.gov/.

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procuremnt: Dr. Jamie Thompson, University of WI

CDNA Library Preparation. Gina Zastrow-Hayes

CDNA Library Preparation. Gina Zastrow-Hayes

CDNA Library Preparation. Gina Zastrow-Hayes

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov

Plate: NOKW80 row: j coluum: 22

High quality sequence stop: 510.

High quality sequence stop: 510.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 971)
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DD - full-length enriched;
                                                                                                                                                                  611 TAGCTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAA
                                                                       AAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAG
                                                                                                                                                                                                                                                                                                          7.8%; Score 78.2; DB 6; Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       851 ATCCTGTATGGAAGAATTAAACGCTGTGAAAATCAA 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="NIH MGC_173"
/note="Vector: pDONR201; Site 1:
LIBR PRIMING - oligo dr; METHÖD
LIBR PROVIDER - Bradfield"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 39 CD388253

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TITLE JOURNAL COMMENT REFERENCE AUTHORS

Query Match

ORIGIN

FEATURES

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                                                                                                                   180 TGTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGT 239
                                                                                                                                                    240 TGGGATAGCGGATGATAAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGG 299
                                                                                                                                                                                                       300 AAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAA 359
                                                                                                                                                                                                                                                        360 ACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAATAA 419
                                                                                                                                                                                                                                                                               420 AATTGCTCCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAATATTGATGC 479
                                                                                                                                                                                                                                                                                                                                                            480 TTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGGTAAAAAACCGTTAGAAGA 539
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BAC library"
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                                                 Query Match
Best Local Similarity 48.7%; Pred. No. 1.8e-05;
Matches 203; Conservative 0; Mismatches 214; Indels 0
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Search completed: August 26, 2005, 06:59:20 Job time : 3914 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 26, 2005, 05:54:23; Search time 2119 Seconds (without alignments) 3112.522 Million cell updates/sec Run on:

US-10-724-972A-2580 1008 Title: Perfect score:

1 ggagtggaatcagtgagagg......gtaaaaaagataataagtaa 1008

Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

7331713 seqs, 3271544945 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:\*

| cgn2\_6/ptodata/1/pubpna/USO7\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO6\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO6\_PUBCOMB.seq:\*
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| cgn2\_6/ptodata/1/pubpna/USO7\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO7\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO7\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO8\_NEW\_PUB.seq:\*
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| cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOM 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

## SUMMARIES

Description	Sequence 2580, Ap	Sequence 34954, A	Seguence 7644, Ap	Sequence 8156, Ap	quence 4404, Ap	equence 35107, A	Sequence 8024, Ap
Dea	S	S	Ø	Se	Se	ß	Se
ID	22 US-10-724-972A-2580	US-10-282-122A-34954	US-10-282-122A-7644	US-09-815-242-8156	US-09-815-242-4404	US-10-282-122A-35107	US-09-815-242-8024
80	22	11	11	6	σ	11	6
% Query Match Length DB ID	1008	993	984	1014	927	525	960
& Query Match	100.0	98.5	56.2	56.0	52.8	30.7	26.3
Score	1008	993	567	564.4	531.8	309.8	265.6
Result No.	7	. 2	e	4	'n	φ	7

. 0

Gaps .. 0

Indels

100.0%; Score 1008; DB 22; 100.0%; Pred. No. 3.1e-162; ive 0; Mismatches 0; 1

Query Match 100. Best Local Similarity 100. Matches 1008; Conservative

Length 1008;

			)				
	ω	264.6	26.2	957	אס	US-09-815-242-4194	Sequence 4194, Ap
	σ	263.2	26.1	957	7	US-10-470-048B-301	301
	10	263.2	26.1	960	13	US-10-282-122A-7949	₩.
	11	222.6	22.1	668	œ	US-08-781-986A-355	Sequence 355, App
	12	222.6	22.1	899	18	US-10-329-624-355	Sequence 355, App
	13	162.2	16.1	242	æ	US-08-781-986A-2556	
	14	162.2	16.1	242	18	US-10-329-624-2556	Sequence 2556, Ap
	15	156.4	15.5	897	11	US-10-282-122A-30706	Sequence 30706, A
	16	149.4	14.8	801	6	US-09-974-300-2066	
	17	143.2	14.2	972	17	US-10-282-122A-9415	Sequence 9415, Ap
υ	18	128		321	6	US-09-815-242-2107	107,
υ	19	128		321	17	US-10-282-122A-4605	Seguence 4605, Ap
	20	125.4	12.4	2115	8	US-08-781-986A-604	04,
	21	125.4	12.4	2115	18	US-10-329-624-604	ď
	22	124	12.3	066	21	US-10-470-048B-318	31
	23	124	12.3	666	16	US-10-278-946-15	
	24	124	12.3	666	7	US-10-967-189-15	
	25	124	12.3	3775	æ	US-08-781-986A-238	Sequence 238, App
	56	124	12.3	3775	18	US-10-329-624-238	33
	27	113.2	11.2	796	17	US-10-282-122A-10009	Sequence 10009, A
	28	103.2		900	17	US-10-282-122A-19870	Sequence 19870, A
	29	95.2		606	σ	US-09-815-242-6372	Sequence 6372, Ap
	30	95.2	4.6	606	17	US-10-282-122A-20621	Sequence 20621, A
υ	31	95.2	9.4	10244	21	US-10-893-671-14	Sequence 14, Appl
	32	79		963	11	US-10-282-122A-17083	
		78.8	7	1026	17	US-10-282-122A-32601	ø
υ	34	78	7.7	431	σ	US-09-960-352-5558	
	35	77.8	7.7	478	13	US-10-021-323-6774	
	36	75.8	7.5	891	17	US-10-282-122A-33236	
υ	37	75.6	7.5	1121	20	US-10-425-115-115706	Sequence 115706,
υ	38	74.2	7.4	1062	20	US-10-425-115-120013	
	39	74	7.3	1214	18	US-10-424-599-102083	
υ	40	74	7.3	1243	20	US-10-425-115-172717	727
U	41	73.8	7.3	421	œ	US-08-781-986A-383	83, 7
υ	42	73.8	7.3	421	18	US-10-329-624-383	œ
	43	72.8	7.2	945	σ	US-09-738-626-375	2,
	44	72.8	7.2	3309400	σ	US-09-738-626-1	•
υ	45	72.6	7.2	446	σ	US-09-960-352-3400	Sequence 3400, Ap

## ALIGNMENTS

RESULT 1
US-10-724-972A-2580
; Sequence 2580, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: RPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
CURRENT APPLICATION NUMBER: US/10/724, 972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
, NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 2580
; LENGTH: 1008
; TYPE: DNA
) ORGANISM: S.epidermidis
02-10-724-97280

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ORGANISM: Staphylococcus epidermidis US-10-282-122A-34954
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Rario
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Fawick, John
APPLICANT: Forsyth, R.
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      GGAGTGGAATCAGTGAGGTTTAAAATTTTAAGTGTAATTGGCTTATTGTTTTTA
                                                                                                                                                                  GTTGTTCTTCATTCATTCATTGATGCCTTAGTTGCTTTAGATGTTAAAACCTGTT
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                                                                                                GATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAAACGT
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US-10-282-122A-34954 ; Sequence 34954, Application US/10282122A

132 192 252 372 240 241 GATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCT 300 9 GCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAA 181 GAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGAATAGCGGAT GATAACAAAAAAATCGTATTATAAACCATTAAGAGATAAAATTGGAAAATACACTTCT GTAGGAACACGTAAGCAACCTAACTTAGAAGAATCAGTAAACTTAAACCAGATTAATT 1 GTGAGAGGTTTAAAAATTTTAAGTGTAATTGGCTTATTGTTTTGTTTTAATTGCAACTGCA 73 GCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAA 133 ATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCTT 193 GAGTATTCATTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGAT GTGAGAGGTTTAAAAATTTTAAGTGTAATTGGCTTATTGTTTTTAATTGCAACTGCA Gaps ö Length 993; Indels Query Match

98.5%; Score 993; DB 17; L
Best Local Similarity 100.0%; Pred. No. 1.1e-159;
Matches 993; Conservative 0; Mismatches 0; 313 셤

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 TCAAGCACGAAGAAGGTACTACGAAAGTACCTAAAACACCCTAAAACGTGTTGTTGTTGTTG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGAACTGAAAAGTITCGATGGAGATTATAATGAAAATATIGATGCTTTTAAAACAATTT 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 AIGGTAAGAAAAACGIAICAIIAAACCAGITAGAGAAAAAAITGGGGAITATACIICIG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CTIGIGGTAATACGGATAATICAAGTAAAAAGAATCATCAACTAAAGATACTATTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 TCAATAAGTATAAAGATGAAATTAAAATTTGATAGAAATCAAAAAGTGCTTCCAGCAGTAG
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56.2%; Score 567; DB 17; Length 9

Best Local Similarity 73.6%; Pred. No. 3.9e-87;

Matches 723; Conservative 0; Mismatches 260; Indels
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-02-09
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; ORGANISM: Staphylococcus aureus
US-10-282-122A-7644
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APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Garn
APPLICANT: Garn
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yau, H.
APPLICANT: You, H.
APPLICANT: BLITRA.034A
CURRENT PILING DATE: 2003-022
CURRENT PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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               301 GTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATT
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US-10-282-122A-7644
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GGAACGATGAGAGGTCTAAAAACTTTTAGTATATTGGGATTAATAGTTGCCTTATTTTA
                                                                             CCTACGATTGAACTGAAAAGTTTCGATGGAGATTAATAAAAAAATATTGATGCTTTTAAA
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US-09-815-242-4404

i Sequence 4404, Application US/09815242

i Patent No. US20020061569A1

i GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
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  AAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGT
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Best Local Similarity 73.1%; Pred. No. 1.1e-86;
Matches 724; Conservative 0; Mismatches 266; Indels 0;
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APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: 2010-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/205, 625
PRIOR APPLICATION NUMBER: 60/205, 625
PRIOR APPLICATION NUMBER: 60/25, 625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Staphylococcus aureus
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US-09-815-242-8156
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US-09-815-242-8156
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
and Prior Application data removed - See File Wrapper or PALM.
R OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Yamamoto, Robert
Forsyth, R.
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Trawick, John
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US-10-282-122A-35107
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                                                APPLICANT: Grant J.
APPLICANT: Grant J.
APPLICANT: Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
FILE REPRENCE: ELITRA.011A
FILE REPRENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 00/209/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
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Pred. No. 3.8e-81;
0; Mismatches 247;
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                                     Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Best Local Similarity 73.4%;
Matches 680; Conservative C
Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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LENGTH: 927
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                                                                                               Length 525;
                                                                                               Query Match 30.7%; Score 309.8; DB 17; Length Best Local Similarity 76.3%; Pred. No. 2.1e-43; Matches 399; Conservative 0; Mismatches 112; Indels
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. HOWard
TITLE OF INVENTION: Identification of Essential Gen
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
                                     TYPE: DNA
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-35107
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Patent No. US20020061569A1
GENERAL INFORMATION:
SOFTWARE: Patentin version 3.1
SEQ ID NO 35107
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US-09-815-242-8024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 ITCAAAAGCTTTAGGTAAAGAAGAAGGTAAAAAAAGCTTAGAAGAACACACATAAGAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 CGCTAAAGCAGTAGGCAAAGAGAAAAAAAGAAGGCGAGAAAAGGTCTGGAAAAAGGATGATAAAAT 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             585 TATCTCAAGAGCAGGTATGTTTAATAATGAAGATACATTTATGGGACAATTCTTAAT 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 GGTTGGATCTAGACCGCAACCGAATATGGAAGTGATAAGTAAATTAAAACCGGATTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 AATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAAACACCCTAAAACGTGTTGTTGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 57.8%; Pred. No. 8.2e-36; Similarity 57.8%; Pred. No. 8.2e-36; Pt. Conservative 0; Mismatches 354;
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 8024
                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(960)
US-09-815-242-8024
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494;
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Best Local S
Matches 494
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APPLICANT: MEINGE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF

TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN

FILE REPERENCE: SONN.035US

CURRENT APPLICATION NUMBER: US/10/470,048B

CURRENT FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603

SOFTWARE: Patentin version 3.1

LENGTH: 957
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                                                                                                                                                                                                                                                                                                                     591 TATCTCAAGAGCAGGTATGTTTATTAATAATGAAGATACATTTATGGGACAATTCTTAAT 650
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                                       411 AATCATGTTAGCGGTACGGGAGATTATAATGCAAATATTGATGCATTTAAAACAGT
                                                                                        TTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAA
                                                                                                                                                                                   AATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGT
GATTGAACTGAAAAGTTTCGATGAGATTATAATGAAAATATTGATGCTTTTAAAACAAT
                                                                                                                                       471 cecrahangcagradecahadaganahadagecenghahacercegahangcardarahan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 301, Application US/10470048B ; Publication No. US20050037444A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Staphylococcus aureus
US-10-470-048B-301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350
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       971
                                            879 TAAGİĞGTIGAANICAAĞĞĞĞTAİTAİLGĞAAĞTĞAAAGTATĞĞCAĞAAĞAAĞTITAĞAAAA 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 TGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 AGAATATAGTTTTGCTGATTATTTAGCAGCATTAGATATGAAACCTGTTGGTATTGCAGA
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         912 CTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTTGTTGA
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Pred. No. 1.2e-35;
0; Mismatches 354; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-02-3
PRIOR PILING DATE: 2000-02-3
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PERESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 4194
                                                                                                                                                                                                                                                                  Sequence 4194, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4194
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                                                                                                                                                                                                                                                                                                                                                                  Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                    972 ATTATCTAAGAAG 985
                                                                                                                                                 939 AATTGCAGAAAAAG 952
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Best Local Similarity 57.89
Matches 493; Conservative
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                                    in Microorganisms
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorgani, FILE REFERENCE: ELITRA.014A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-05-26
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Pred. No. 2.1e-35;
0; Mismatches 408;
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Best Local Similarity 55.9%;
Matches 524; Conservative (
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              ACACCCTAAACGTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGA
                                    TGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAAATCGTATTATTAAACCATTAAG
                                                                                                                                                                     TATGAAACCTGTTGGTATTGCAGATGATGGCACCACTAAAAATATAACAAAGTCAGTAAG
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Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Tyekind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
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621 TACATTTATGGGACAATTCTTAATTAAAATGGGTATTCAACCTGAAGTCACAAAAGACAA 680
                                                                                                                                     741 TGCCAATATCAATCCAAAAGTTATGATTTTAGCCACTGACGGAAAACGGACAAAAA--- 797
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Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                 681 AACTACGCATGTTGGTGAACGCAAGGGTGCTCTTATATATTTTAAATAATGAAGAACT
                                561 GTTAAAATCTGCATTGCATTCGGTATCTCAAGAGCAGGTATGTTTATTAATAATGAAGA
                                                                  648 CICTIAIGITGGICAATICCIAAGICAACIAGGITITIAAAGAAGCATIAAGIGAIGAIGI
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELEPANE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Scier
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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nucleic acid
EDNESS: double
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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TILLE OF INVENTON: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 966
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
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COFTWARE: ACIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION NUMBER: 08/956,171
APPLICATION NUMBER: 08/956,171
FILING DATE: Occober 20, 1997
APPLICATION NUMBER: 06/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
  Pred. No. 1.6e-28;
0; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 96,789
TELECOMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: January 3, 1997 ATTORNEY/AGENT INFORMATION:
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Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
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Best Local Similarity 74.89
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rockville
STATE: Maryland
COUNTRY: USA
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Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                             DB 18; Length 668;
                                                                                                                                                                                           22.1%; Score 222.6; DB 18; Length 74.8%; Pred. No. 1.6e-28; ive 0; Mismatches 94; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOPTWARE: ASCII Text
                                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 355:
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INFORMATION FOR SEQ 1D NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                               Best Local Similarity
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Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387
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MUEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OOFRATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 5, 1996
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                          Score 162.2; DB 8;
Pred. No. 2.3e-18;
0; Mismatches 50;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPA: (301) 309-8512
TELEPA: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                            Query Match 16.1%;
Best Local Similarity 79.3%;
                                                                                                                                                                                                                                                                                                                                Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
STATE: Maryland
                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-781-986A-2556
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LENGTH: 897
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FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
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                                                                                                                                                                                                                                               16.1%; Score 162.2; DB 1
79.3%; Pred. No. 2.3e-18;
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: PB248PID1
RELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                 ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2556:
105-10-329-624-2556
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                                                                                                                              LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Malone, Cheryl
Haselbeck, Robert
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                Best Local Similarity 79.3
Matches 191, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-282-122A-30706
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423 acaaaaahrcggrgartrarraggraaarcaaaagaaargcaagggggrarrgcaaaaca 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 AGATTTGATCATTGCCGATGATAATCGCCATTCTGCCGTCTATGAAGAACTCAAAAAAT 362
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                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 30706
PRIOR APPLICATION NUMBER: 60/253,625
RRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
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US-10-282-122A-30706
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Best Local Similarity 51.9%;
Matches 454; Conservative
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716 GITIBAGIBAGIBICITBAAGGACCITACITBCAAATGAACACTGAAACTITAICICAAG 775
                                          535 GCGATGCCGAAAACGGTGAATCCGTCAATATTAAAATGACGCTCGAACAGCTGCTTGAGA 594
                                                                                                                                595 pagarcccgacgriatrerccrgargacgagagagagagaraangrcgargagacgga 654
                                                                                                                                                                                                                             655 AAAGACCGATCGAAAAGATCCTCTTTGGAAAAGCTCAGCGCAGTCAAAAACGGCAAGG 714
                                                                                                                                                                                                                                                                        TTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAA 952
                                                                                                                                                                                                                                                                                                                     715 Tritargaagccgacadarrcgccrggrcgcrccgacgcagcarrgacggagcadagagc 774
                                                                                        776 TGAATCCTGAGCGTATGTTCATAATGAC---AAACAAAGCAAGTTCTAACGAACCTTCAC
                                                                                                                                                                                  833 TAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTG
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-02
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-282-122A-9415
Sequence 9415, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                  TGATGGATGAAATCGATCA 793
                                                                                                                                                                                                                                                                                                                                                                     TGGCAAAGAACTTGTTGA 971
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SEQ ID NO 9415
LENGTH: 972
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US-10-282-122A-9415
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Yamamoto, Robert
Forsyth, R.
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Wall, Daniel
Trawick, John
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                                   176 AACGTGTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAAC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGGAAAATACACTICTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAAC 355
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       903 AGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTTGGGATAGCGGATGATAACAAAAAAATCGTATTATTAAAACCATTAAGAGATAAAA
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                                                                                                                                                                                                                                                Sequence 2066, Application US/09974300
| Patent No. US20020146721A1
| GENERAL INPORMATION:
| APPLICANT: Berka. Randy M. APPLICANT: Clausen, ID Groth
| TITLE OF INVENTION: Machods For Monitoring Multiple Gene
| TITLE OF INVENTION: Expression
| FILE REFERENCE: 10085.500-US
| CURRENT APPLICATION WUMBER: US/09/974,300
| CURRENT APPLICATION NUMBER: 2001-10-05
| PRIOR PILING DATE: 2000-10-06
| PRIOR PLILING DATE: 2000-10-06
| PRIOR PLILING DATE: 2001-3-27
| NUMBER OF SEQ ID NOS: 8481
| SOFTWARE: PESESSQ for Windows Version 4.0
| SEQ ID NO 2066
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0; Mismatches 376;
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                                                                                               ACTIGITGAATTATCTAAGAAAGATAGTAAAAAA 996
                                                                                                                                          864 AGICCAAGACITIGIAACGAAAICCGCCAAAIAA 897
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Pred. No. 4.8
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; ORGANISM: Bacillus licheniformis
US-09-974-300-2066
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Best Local Similarity 51.8%;
Matches 414; Conservative
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                                                                                                                                                                                                                  85 AATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAA 144
                                                                                                                                                                                                                                                                                  67 GAGGAGAAAAAAAAAAAAAAGCGGACAATAAAAATCAAGCTATAACAATTAAACACGCT 126
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                                                                   25 AAAATITIAAGIGIAAIIGGCTIAIIGITITGTITIAAIIGCAACIGCAGCAIGIGGAAAI 84
                                                                                                                                       7 AAAATTCTCAGATTTTCATAGTAGTTTTTCTATTCGCTGTTGGATGCGGACAGCAAAAA 66
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       Matches 308; Conservative
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US-09-815-242-2107/c
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132 AATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCT 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 GGTTGGATCTAGACCGCAACGGAATATGGAAGTGATAAGTAAATTAAAACCGGATTTGAT 32
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Pred. No. 1.7e-12;
0; Mismatches 85
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CURRENT PEDLICATION NUMBER: US/10/282,122A

CURRENT PELING DATE: 2003-02-20

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PELING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SSCTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2107
LENGTH: 321
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                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-2107
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 67.8%;
Matches 179; Conservative
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Ohlsen, Kari
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Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Wall, Daniel
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LENGTH: 2115 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTC 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 604, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVORTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 TGATGGCAGCACTAAAAATATAAACAAAGTCAGTAAGAGATAAGATTGGGGCATATGAATC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 TGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGA
                                                                                                                                                                                                                                                          Gaps
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 4605
LENGTH: 321
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                                                                                                                                                                                                                                                                                         132 AATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGT
                                                                                                                                                                                                                     Length 321;
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WEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: PF VECTER 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
                                                                                                                                                                                                                     Score 128; DB 17;
Pred. No. 1.7e-12;
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 TATTGCTGATAATAATAGACACAA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 604:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 CATTGCAGATGTTAGCAGACATAA
                                                                                                                                                              ORGANISM: Staphylococcus aureus US-10-282-122A-4605
                                                                                                                                                                                                                   Query Match
Best Local Similarity 67.8%;
Matches 179; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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US-08-781-986A-604
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SEQUENCE CHARACTERISTICS:

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Sequence 604, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                             61 AAGGCGAGAAAGCGTCTGGAAAAGCATGATAAAATATTAGCGGAGATTAGAAAAAATTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AACAGAGTACGTTAAAATCTGCATTTGCATTCGGTATCTCAAGAGCAGGTATGTTATTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     818 CTAACGAACCTTCACTAAAAGAACTAGAAAAAAAATCCTGTATGGAAGAAATTAAAACGCTG 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ACAAAAA-----TAGAACGAAATTCATTGATCCTGCAGTTTGGAAATCATTAAAAGCTG 414
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                                                                                                                      Length 2115;
                                                                                                                      Score 125.4; DB 8; Length
Pred. No. 7.5e-12;
1; Mismatches 247; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                      Query Match
Best Local Similarity 53.2%;
Matches 289; Conservative 1
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STATE: Maryland
COUNTRY: USA
TYPE: nucleic acid
STRANDEDNESS: double
; TYPE: nucleic aci
; STRANDEDNESS: dou
; TOPOLOGY: linear
US-08-781-986A-604
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Sequence 318, Application US/10470048B Publication No. US20050037444A1 GENERAL INFORMATION:
                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-470-048B-318
                       US-10-470-048B-318
                                                                                                                                                                     SEQ ID NO 318
LENGTH: 990
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Pred. No. 7.5e-12;
1; Mismatches 247;
                                                                                                                                                                  TELECOMUNICATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: P8248PID1
TELECOMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAK: (301) 309-8439
FORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                             APPLICATION NUMBER: US/10/329,624 FILING DATE: 27-Dec-2002 PRIOR APPLICATION DATA:
                                                                                APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 604:
                                                                                                                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: double
                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.2%;
Matches 289; Conservative
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APPLICATE: MEINEE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF ITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
SOFTWARE: PATENTING DATE: 2003-07-25
SOFTWARE: PATENTING PATE: 2003-07-35
SOFTWARE: PATENTING PATE: 2003-07-35
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662 ALTIAGGAITCAAACGIAATAAAGACTIACAAAAACAAGTIGAIAATGGTAAAGAIAITA
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TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: PB461USD2
CURRENT APPLICATION NUMBER: US/10/967,189
CURRENT PILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US 10/278,946
PRIOR FILING DATE: 2002-10-24
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 60/078,682
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-06-07
PRIOR PILING DATE: 1998-06-07
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50.7%; Pred. No. 1.1e-11;
tive 0; Mismatches 380;
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; ORGANISM: Staphylococcus aureus
US-10-967-189-15
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SEQ ID NO 15
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Matches 412; Conservative
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TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: P846(1USD1
CURRENT APPLICATION NUMBER: US/10/278,946
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US/9/830,217
PRIOR APPLICATION NUMBER: PCT/US99/06199
PRIOR APPLICATION NUMBER: PCT/US99/06199
PRIOR PILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 60/08,682
PRIOR FILING DATE: 1998-03-20
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                                                                                                                                                           776 aarcagarccaaargcgaagargcrgcarra 807
                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/10278946 Publication No. US20030153733A1 GENERAL INFORMATION:
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7 ORGANISM: Staphylococcus aureus
US-10-278-946-15
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Best Local Similarity 50.7%;
Matches 412; Conservative
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US-10-278-946-15
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TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA 326
                                                        GCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAA 386
                                                                          318 TGCACCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCAAAAGT 377
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TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                               378 TAGAAATGAAAAGTTTACGATCAATTATCTAAAATCGCACC-----AACAG
                                                                                                                                                                            TTTCGATGGAGATTATAATGAAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAG
                                                                                                                                                                                                          Tricracidatacagritricaaarricaaagaracaacraagritaarggggaaagcritrag
                        258 ACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAAGAACC
                                                                                                                   387 TAGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG
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ZID: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
AMDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
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APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 25
US-08-781-986A-238
; Sequence 238, Application US/08781986A
; Publication No. US20030054436A1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTAAAATGCTTGTTGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA 326
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                                                                                                                                                                                                                                                                                                                                   Length 3775;
                                                                                                                                                                                                                                                                                                                            Score 124; DB 8; Length 37 Pred. No. 1.5e-11; 0; Mismatches 380; Indels
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                               TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   Query Match 12.3%;
Best Local Similarity 50.7%;
Matches 412; Conservative (
                                                                                                                                                   3775 base pairs
                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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565 586 622 646 682

446 466 505 526 703

742

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APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Va, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-36
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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                     GCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAA
                                                                 360 TGCACCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCAAAAGT
                                                                                                                                                                        420 TAGAAATGAAAAGTTTACGATCAATTATCTAAAATCGCACC-----AACAG
                                                                                                                                                                                                                                                                         467 TTTCTACTGATACAGTTTTCAAATTCAAAGATACAACTAAGTTAATGGGGAAAGCTTTAG
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                                                                                                                      TAGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG
                                                                                                                                                                                                                          TTTCGATGGAGATTATAATGAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAG
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
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APPLICANT:
APPLICANT:
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                                                                                                              Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA 146
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COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIORICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PlD1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 238: US-10-329-624-238
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Scie
STREET: 9410 Key West Avenue
                  Sequence 238, Application US/10329624
Publication No. USZ0040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8439
INPORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 Dage pairs
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STRANDEDNESS: double
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Best Local Similarity 50.7
Matches 412; Conservative
                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
US-10-329-624-238
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APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Porsyth, R.
APPLICANT: Porsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFRENCE: ELITRA.0184A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/22/22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
Remaining Prior Application data removed - S
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10009
                                                                                                                                                                                                                                                                                                    Score 113.2;
Pred. No. 7e-
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Best Local Similarity 57.6%;
Matches 227; Conservative
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AACTGAAAAGTTTCGATGGAGATTATAAATGAAAATATTGATGCTTTTAAAACAATTTCAA 496
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                      PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PELING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PELING DATE: 2001-02-16
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PRIOR PELING DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
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Patent No. US20020061569A1
GENERAL INFORMATION:
60/207,727
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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Best Local Similarity 52.9°
Matches 222; Conservative
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APPLICANT:
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51.7%; Pred. No. 8.4e-07;
Live 0; Mismatches 203; Indels
Sequence 20621, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Kari
APPLICANT: Oblisen, Kari
APPLICANT: Wall, Daniel
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Matches 217; Conservative
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APPLICANT: FORSEYT, R. APPLICANT: APPLICANT: APPLICANT: APPLICANT: Xu, H. APPLICANT: Xu, H. Identification of Essential Genes in Microorganisms of TITE OF INVENTION: ELITRA.034A CURRENT ELITRA.034A CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/1206, 848
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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51.7%; Pred. No. 8.4e-07;
iive 0; Mismatches 203;
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SEQ ID NO 20621
LENGTH: 909
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Matches 217; Conservative
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US-10-282-122A-20621
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Similarity 47.1%;
12; Conservative (
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US-10-282-122A-17083
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Best Local 5
   CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                        Length 10244;
                                                  APPLICANT: Levy, Stuart, et. al.
TITLE OF INVENTION: NIMR COMPOSITIONS AND THEIR METHODS OF USE
FILE REFERENCE: PKZ-043
CURRENT APPLICATION NUMBER: US/10/893,671
CURRENT APPLICATION NUMBER: US/09/801,563
FRIOR APPLICATION NUMBER: US/09/801,563
FRIOR PELING DATE: 2004-07-15
FRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 10244
                                                                                                                                                                                                                                                                                                                                                                                                                             137 AGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGT
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.6e-06;
0; Mismatches 203;
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Sequence 14, Application US/10893671
Publication No. US20050064527A1
GENERAL INFORMATION:
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APPLICANT: Aamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                        Query Match 9.4%;
Best Local Similarity 51.7%;
Matches 217; Conservative
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Forsyth, R.
                                                                                                                                                                                                                                                                                                    ; ORGANISM: Escherichia coli
US-10-893-671-14
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Carr, Grant
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APPLICANT:
APPLICANT:
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Pred. No. 0.00049;
PRIOR FILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,635
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-12-26
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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Sequence 5558, Application US/09960352

Sequence 558, Application US/09960352

Sequence 558, Application US/09960352

GENERAL INFORMATION:

APPLICANT: Wasten, Wesley C.

APPLICANT: Mathialagan, Nagappan

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION NUMBER: US/09/960,352

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

SEQ ID NOS: 15112

SEQ ID NOS: 15112
198 TCAAGGCACCACTGAGATCCCTGCTCACCACAAAAAGTGGTTGTGATGAACATGGAAAC 257
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                                                                                                          204 TGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAA
                                                                                                                                                                         258 ACTIGATATIGITGATGCICTIGGCGTACCTGTTGTTGGCCTACCACAAACAACGTCCA
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Pred. No. 0.00059;
0; Mismatches 170; Indels
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; OTHER INFORMATION: Clone ID: 24-LIB3057-024-Q1-K1-F7
US-09-960-352-5558
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Best Local Similarity 51.4%;
Matches 180; Conservative
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US-09-960-352-5558/c
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
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                                                                                                             612 Trraagigratriggrgaagaricaagarriagrararraraaragrrirga 671
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                                             TITGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 32601, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ollsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
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SEQ ID NO 32601
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
Matches 271; Conserv
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APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21/522741B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT APPLICATION NUMBER: US 60/255, 619
PRIOR PLING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 6774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 ACCAGATITAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAATAA 419
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553
                              TTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGA
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CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
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49.3%; Pred. No. 0.00065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(478)
CHER INFORMATION: unsure at all n locations
CTHER INFORMATION: Clone ID: LIB3828-010-Q1-N6-E1
US-10-021-323-6774
                                                                                                                                                                          Sequence 6774, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 49.3 Matches 202; Conservative
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NAME/KEY: unsure
LOCATION: (1)..(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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APPLICANT: Foreyth, R.
APPLICANT: Ku, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITIE OF INVENTION Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-03-21
PRIOR PRIOR PLICATION NUMBER: 60/291,078
PRIOR PLICATION NUMBER: 60/200,33
PRIOR PLILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR PLILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
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PRIOR PLILING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 78614
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47.7%; Pred. No. 0.0017;
tive 0; Mismatches 242;
Sequence 33236, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Pseudomonas syringae
US-10-282-122A-33236
                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: 2yskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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SEQ ID NO 33236
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Forsyth, R.
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Best Local Similarity 47.74
Matches 221; Conservative
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Sequence 120013, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: LASORA, Thomas J.
APPLICANT: APPLICANT: About, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
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                                                                                                                          795 CATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCC
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                                                                                  314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA
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Pred. No. 0.0033;
0; Mismatches 168; IndelB 0;
                                                                                                                                                                                                             855 TGTATGGAAGAATTAAACGCTGTGAAAAATCAACGTGTTGATA 898
                                                                                                                                                                                                                                                    489 actacataatagatcaaaaaaccaaacatacaaaacctgata 446
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US-10-425-115-120013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(1062)
OTHER INFORMATION: unsure at all n locations
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7.4%;
Best Local Similarity 51.0%;
Matches 175; Conservative C
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ORGANISM: Zea mays
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US-10-424-599-102083
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Bequence 115706, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040212A1
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 115706
LENGTH: 1121
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                                                                                                        413 TGATCGGCATGGCGCTGGGCAAAAGGCCCGGAGATGCAGGGCGCGAATCGCAGAAAACCGTC 472
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                                                                                                                                                  548 AGAAATTGAAGAATATAAAAAGAAATAACTATGGATAAAAA 590
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US-10-425-115-115706
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OTHER INFORMATION: ungure at all n locations
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US-10-425-115-115706/c
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ORGANISM: Zea mays
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Matches 288;
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                                                                                            es and Other Molecules Associated With for Plant Improvement
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Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: AROSA, Thomas J.
APPLICANT: AROSA, Thusa
APPLICANT: AROSA, VORGWei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21,8
FILE REFERENCE: 38-21,8
FILE REFERENCE: 38-21,8
FILE REFERENCE: 36-22,8
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 17217
LENGTH: 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                           314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA
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                                                                                                                                                                                                                                                                                                                                  Length 1214;
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Pred, No. 0.0037;
0; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 TIGAAGAATATAAAAAAAAAATAACTATGGATAAAAATCAAAA 596
                                  APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof for P
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_63198C.1
US-10-424-599-102083
                                                                                                                                                                                                                                                        LOCATION: (1)..(1214)
OTHER INFORMATION: unsure at all n locations
Sequence 102083, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.7%;
Matches 167; Conservative
                                                                                                                                                                                                                ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
US-10-425-115-172717/c
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                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(1
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ACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTTGTTG 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 TITCAAAAGCTTTAGGTAAAAAAAAAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAAA 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAA
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                                                                                                                                                                          Gaps
                                                                                                                                                                          ъ,
                                                                                                                                 Length 1243;
                                                                                                                                                                          0; Mismatches 422; Indels
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                                                                                                                                 Query Match 7.3%; Score 74; DB 20; Best Local Similarity 43.7%; Pred. No. 0.0037; Matches 330; Conservative 0; Mismatches 422
                                                                         ) OTHER INFORMATION: Clone ID: MRT4577_89100C.1
US-10-425-115-172717
NAME/KEY: unsure
LOCATION: (1)..(1243)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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